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Run on:	<pre>January 9, 2003, 19:57:20 ; Search time 2487.88 Seconds (without alignments) 7673.783 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-09-581-500B-12 656 1 gccaacaaaacaaaatgaaatcccaccgcgagaccccgcga 656
Scoring table:	IDENTITY_NUC Gapop 10.0, Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of 1	hits satisfying chosen parameters: 4109280
Minimum DB seq Ie Maximum DB seq le	length: 0 length: 200000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:* 1: 9b_ba:* 2: 9b_htg:* 4: 9b_om:* 5: 9b_ow:* 6: 9b_pa:* 7: 9b_ph:* 8: 9b_pl:* 8: 9b_pl:* 10: 9b_pl:* 11: 9b_sp:* 12: em_fu:* 13: em_htg.hu:* 13: em_htg.hu:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PAT 07-SEP-2000	Euteleostomí;	. Olio
linear	human. Homo sapiens Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	1 (bases 1 to 656) Del-Favero, J., Raeymaekers, P. and Van Broeckhoven, C. Mood disorder; WO 9932643-A 12 01-JUL-1999;
bp DNA 2643.	Craniata;	and Van E L-1999;
AX021006 656 bp Sequence 12 from Patent W09932643. AX021006	Chordata;	1 (bases 1 to 656) Del Teavero, J., Raeymaekers, P. and Va. Mood disorder gene Patent: WO 9932643-A 12 01-JUL-1999;
AX021006 Sequence 12 from Patent AX021006	ens ; Metazoa;	1 (bases 1 to 656) Del-Favero, J., Raeym Mood disorder gene Patent: WO 9932643-A
AX021006 Sequence AX021006	human. Homo sapiens Bukaryota; Me	1 (bases Del-Faver Mood diso Patent: W
RESULT 1 AX021006 LOCUS DEFINITION ACCESSION	KETWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL

ALIGNMENTS

source

FEATURES

BASE COUNT

ORIGIN

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181 241 301

421 421 481

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Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dases 1 to 19195)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Cabing, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Castle, M., Ferreira, P., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Grant, G., Hagos, B., Heaford, A., Horton, L., Karate, M., Grant, G., Hagos, E., Heaford, A., Horton, L., Kleib, J., Landers, T., Johnson, R., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McTarthy, M., McDara, P., McGurk, A., McKernan, K., McDeeters, R., Marquis, N., Maylor, J., Norman, C. I., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Spencer, B., Stange-Thomann, N., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stolaman, A., Triqillo, J., Vassillev, H., Vell, R., Vo, A., Wilson, B., Way, K., Wyman, D., Ye, W., Vassillev, H., Vell, R., and B., A., an
                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barker, J., Barda, N., Beckerly, R., Benn, J., Brown, A., Gastle, A., Galorgel, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Doonlan, L., Doyle, M., Ferreira, P., FitzHudh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardynad, C., Gilbert, D., Gardyna, Branke, R., Mardord, M., McFwan, P., Morton, M., Mordand, J.C., Jones, C., Kann, L., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Marduis, N., Mortis, W., Morrow, J., Mychalecky, J., Mardin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Then, C., Then, C., Massiliev, H., Vo, A., Magner, A., Then, C., Then, C., Massiliev, H., Vo, A., Magner, A., Then, C., Then, C., Massiliev, H., Vo, A., Magner, A., Then, C., Massiliev, H., Vo, A., Magner, A., Then, C., Mark, M., Magner, A., Magner, A
                                                Lander, E., Allen, N., Anderson, M.,
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 16, 2000 this sequence version replaced gi:6514043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
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Center clone name: 793_J_2
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/rpt_family="L1MA4A"
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/clone="RP11-793J2"
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/rpt_family="L1M2"
474. .708
/rpt_family="L1"
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/rpt_family="L1"
1351. .16??
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JOURNAL
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JOURNAL
        REFERENCE
                                                AUTHORS
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BROBCKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191395)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO09802 191395 bp DNA linear PRI 17-FBB-2
Homo sapiens chromosome 18, clone RP11-793J2, complete sequence.
ACO09802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IGATTAGTATCCTTATCAGGAGCAATTTCAGAAATGTTTGGGTGGACGTCTAACTTACG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AAAAACCACCCTCCAAGGACCAGGCACTGGCCCTCTCTCCGGTGCCCACAGACATCCACA
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.5%; Score 652.6; DB 6; Best Local Similarity 100.0%; Pred. No. 8.1e-148; Matches 656; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                               96
                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                               208 g
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/rpt repeat_region comp /rpd repeat region 1704	-		repeat_region 1822	•	•	/rpi repeat_region 2189 /roi	repeat_region com	repeat_region compression comp			repeat_region 558	repeat_region 2603	repeat_region 263		repeat_region 269		Query Match Best Local Similarity Matches 649: Conserv	GCCAACA	98274	Qy 61 TGATTAGTATCCTT	Db 98214 TGATTAGTATCCTT	Oy 121 TGGAGTCAAACGTG		Db 98094 AAAACCACCTCC	Qy 241 CAGGCCCAAAGAAT	Db 98034 CAGGCCCAAAGAAT	OY 301 CCGGAAGCCTTGCC	361	97
16321687	1688 . 2207 // Tpt_family="Lika4A" // Commily="1700" 1770	Comprehensis, 17.0) /note="Single-stranded terminator coverage." 22082215	/rpt_family="(TATATG)n" 294. 2548. 2548.	/rpc_ramilyindia_r/rpc_remil(26492991) /rpc_family="MER2"	29923475 // rpt_family="LIME"	Complement(4330443/) /rpt_family="FRAM" 44384567	/rpt_family="(TA)n" 4599. 4959	/rpt_family="AT_rich" 4982. 5151 /rrt family="/mbmmg.n"	5144. 5311 /rpt_family="(TATAA)"	52575441 //rt_family="(TA)n"	54445242 Tryt_family="AT_rich" F=22	3535. 20108 /rpt_family="(TTATA)n" 5742 5907	/rpt_family="(TTATA)n" complement(59666047)	/rpt_family="FRAM/FAM" 6682 6703	/rpt_family="AT_rich" 7034. 7933 7nt family="AT_rich"	79358006 /	/IPC_Lamily="Alu:" 8009.	/rpt_family="aT_rich" 9216. 9496	/rpt_family="Alusx" 94979520	/rpt_family="(CAAA)n" 9961_10264 /	<pre>'IPL_Id#L1y='Alu! complement(10837, .10840) /note="\$\sqrt{s}\ind\cdots\rangle\cdot\rangle\cdots\rangle\cdots\rangle\cdots\rangle\c</pre>	complement(1115611515) /rpt_family="THEIC" 11856 11007		1 \		.		, ,,,,	/rpt_fa
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Db 182575 GTGGGGGTCGCCCTGGCACCAGCGGGGGTCCCAAGCCCCACCGGGAGACCGGGGAA 182520
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-589E3"
/clone_lib="RPCI-11 Human Male BAC"
62849 a 38924 c 38683 g 57534 t 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 646.2; DB 2;
Pred. No. 3.8e-146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .198291
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.5%;
98.8%;
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Matches 648; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signature, B., Linton, L., Nusbaum, C., Iander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Brown, S., Bugualayth, L., Boukhagiter, B., Brown, A., Burket, G., Collins, S., Congel, Y., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, R., Diaz, J.S., Dadge, S., Domino, M., Doyle, M., Perreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardt, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Kanth, J., Lañocque, K., Lamazares, R., Landers, T., Tehocaky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McDenson, P., McGurk, A., McKennan, K., McPheeters, N., McTarth, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Maylor, J., Norman, C.H., O'Connor, T., O'Connell, P., O'Neil, D., Ollyar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollvar, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Voasilley, H., Viel, R., Voa, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Wasilley, H., Viel, R., Voa, Wilson, B., Wu, X., Wyman, D., Ye, W. J., L., Shanission on May 24, 2001 this sequence version replaced gi:13560423.

All repeats were identified using Repeatmasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC067875 199291 bp DNA linear HTG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-589E3 map 18, *** SEQUENCING
IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         97734 GGCGGCAGGAACTAGGAGAATGACGCGGCAGGCGGCCGGGAAAGAGAGTCGCGGGGCT 97675
                                                                                      97854 CCAGGTACCGGGGGGGGGGCAGGCAGGTGCCCAGGTTCCCGGGAGGCCACCTCTTCC 97795
                                                                                                                                                                                                     ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                     CCAGGTACCGGGGGGGGCACGCAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
                                                                                                                                                                                                                                                                                   541 GGCGGCCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCT 500
                                                                                                                                                                                                                                                                                                                                                                                                                             481 CTGGAGTGCGTGAGAGGGAAGGGAAGGGAAGGCCAGAGCCAGGAATCAGAGCGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                  GTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCGCGAGACCCCGCGA 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACO67875.7 GI:14193020
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 198291)
Birren,B., Linton,L., Nusbaum,C. and Lander,B.
Homo sapiens chromosome 18, clone RP11-589E3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smit, A.F.A. & Green, P. (1996-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone name: 589_E_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 198291)
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AC067875/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
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JOURNAL
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                  601
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AUTHORS
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KEYWORDS
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Db 183175 GCCAACAAACAAATGAAATGAAATAAGACCTGGGATGTATTTTTTGGCCAAGGCAATTAGAAAA 183116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 182875 CCGGRAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGAGGAATAGTCAA 182816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 183115 TGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 183056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGGAGTCAAACGTGAATCAACGGTGAAAAAGGACAATAGCCAATGTGTACACTTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AAAAACCCCTCCAAGGACCAGGCACTGGCCCTCTCTCCGGTGCCCACACATCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CAGGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 182935 CAGGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGTACCGGGCGGGCCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182755 CCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 CTGGAGTGCGTGAGAGGGGAAGGGAAGGAAGGCAAGCCAGAAGCAAGTCAGAGCGAGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 GGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 198291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 others
                                                                                                                             15 198291: contig of 69487 bp in length. Location/Qualifiers
                      38269 38368: gap of 100 bp 38369 109704: contig of 71336 bp in length 109705 109804: gap of 100 bp 109805 128704: contig of 18900 bp in length 128705 198291: contig of 69487 bp in length.
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8268: contig of 38268 bp in length
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ORGANISM

SOURCE

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

AC090224/c DEFINITION

ACCESSION VERSION KEYWORDS

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Db 147829 CAGGCCCAAAGAATCAGGGAIIGCACAAGCCAGAGCAAICGAACGGIICTGAGTCAICIG 147770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 CAGGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGTAAGAATCTACAAAGGAGGAATAGTCAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCCAACAAACAAATGAAATAAGACCTGGGATGTATTTTTTGGCCAAGGCAATTAGAAAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 201734;
                                                                                                                                                                                                            * 4974 51333: contig of 100 bp

4974 51333: contig of 1650 bp in length

51394 51493: gap of 100 bp

51494 74531: contig of 23038 bp in length

74532 74531: gap of 100 bp

74532 127711: contig of 53079 bp in length

127711 127810: gap of 100 bp

127811 20174: contig of 73924 bp in length

1. 201724: contig of 73924 bp in length

1. 201724
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46769 46868: gap of 100 bp
46869 47961: contig of 1093 bp in length
47962 48061: gap of 100 bp
48062 49643: contig of 1582 bp in length
                                                    100 bp
1485 bp in length
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/clone="RR11-693A18"
/clone_lib="RPCI-11 Human Male BAC"
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Eg (Dasses 1 to 201734)

Birnen, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Birnen, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Birnen, M., Campopiano, A., Chopel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Ginde, S., Goyette, M., Grand-Pierre, M.,

Gardyna, S., Ginde, S., Goyette, M., Grand-Pierre, M.,

Hagos, B., Heaford, A., Hortcon, L., Hullme, W., Illev, I., Johnson, R.,

Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,

Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,

Marquis, N., Matthews, C., Norathy, M., McKenan, K.,

McChano, T., Nopuen, C., Norathy, M., McKenan, K.,

Murphy, T., Naylor, C., Norathy, M., McKenan, K.,

Nurphy, T., Naylor, J., Nguyen, C., Noratho, C., Rotta, R.,

Riaback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Karback, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,

Submitted (17-FBE-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA

On May 23, 2001 this sequence version replaced gi:1361272.

All repeats were identified using RepeatMasker: html

http://ftp.genome.washington.edu/RW/RepeatWasker:html

http://ftp.genome.washington.edu/RW/RepeatWasker:html
                                                                                      AC090224 201734 bp DNA linear HTG 23-MAY-2001 Homo sapiens chromosome 18 clone RP11-693A18 map 18, WORKING DRAFT SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201734)
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Insert size: 201034; sum-of-contigs
Insert size: 201034; sum-of-contigs
Quality coverage: 11.3 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
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AC090224.4 GI:14190716
HTG: HTGS_PHASE1; HTGS_EVLLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases I to 191793)
Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Hombished only in Database (2000)
2 (bases 1 to 191793)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                           147589 CTGGAGTGCGTGAGAGGCGAAGGAGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAA 147530
DD 147769 CCGGAAGCCTTGCCCTCAATCAAGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAA 147710
                                                                                                         LYJ bp DNA linear HTG 30-MAY-;
Homo sapiens chromosome 18 clone RP11-693A18 map 18q22, WORKING
DRART SEQUENCE, 54 unordered pleces.
AP001897
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Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                                                                 480
                                                                                                                                                                                                                                                                              CTGGAGTGCGTGAGAGAGGGAAGGAAGGAAGGCCAGAAGCAGGAATCAGAGCGAGGCAAA 540
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Fax:81-42-778-9924)
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Homo sapiens DNA, clone:RP11-693A18.
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AUTHORS
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AP001897
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are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence updated (26-May-2000).
* NOTE: This is a "working draft' sequence. It currently se consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
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f 5221 bp in length
100 bp
f 4913 bp in length
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2062 bp in length
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70897 172731: contig of 1835 bp in length
72832 173831: gap of 100 bp
72832 174664: contig of 1633 bp in length
7465 174564: gap of 100 bp
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2159 bp in length
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4356 bp in length
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6602 bp in length
in length
               53200: contig of 7457 bp in 53300: gap of 100 to 10
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86515: contig of 4:
86615: gap of 100
6 90836: contig of 4:
                                                                                                                                                                                                                                                             23: gap of 10
71725: contig of 6
25: gap of 10
77046: contig of 5
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Diagnosis of diseases associated with the immune system
Patent: Wo 0200928-A 1457 03-JAN-2002;
Epigenomics AG (DE)
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                                                                                                    ch 98.0%; Score 643; DB 2; Length 191793; 11 Similarity 98.5%; Pred. No. 2.3e-145; 646; Conservative 1; Mismatches 9; Indels 0;
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174565 175680: contig of 1116 bp in length 175681 175780: gap of 1100 bp 176918: contig of 1138 bp in length 176919 177018: gap of 100 bp 177019 178822: contig of 1804 bp in length 178823 178922; gap of 100 bp
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AX346386
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Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission.

Buirect Submission.

Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail: hattori@gsc.riken.go.jp,
UKL: http://ngp.gsc.riken.go.jp/, Tel:81-42-778-9923,

Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                                                                                        On May 30, 2000 this sequence version replaced gi:7288199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 0.990329
Consensus quality: 162162 bases at least 040
Consensus quality: 175309 bases at least 040
Consensus quality: 181326 bases at least 030
Insert size: 184151; sum-of-contigs
                                                                                                                                                                                                                                  Center: RIKEN Genomic Sciences Center(GSC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4730 TTAGTAFTTTATTAGGAGTAATTTTAGAGAATGTTTGGGTGGACGTTTAATTATAGGG 4789
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                                                                                                                                                                                                                                                       4670 AATAAATBAAATGAAATAAGATTTGGGATGTATTTTTTGGTTAAGGTAATTAGAAAATGA 4729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 GAGTGCGTGAGAGGAAGGGAAGGCAAGACCAAGAGAATCAGAGCGAGGCAAAGGC 543
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
1 187 c 2897 g 6648 t
                                                                                                                                                                                                                                                                                                 64 ITAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAGTGG 123
                                                                                                                                                                      Gaps
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                                                                                                                           DB 6; Length 13202;
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                                                                                                                           Score 441.6; DB 6; Length Pred. No. 1.5e-96; 1; Mismatches 133; Indels
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1458 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
1. .13202
/organism="synthetic construct"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1458 from Patent WO0200928. AX346387
                                                                                                           169799. 173554.
| note="assembly_fragment" | 173555. 175564 |
| note="assembly_fragment" | 17565. 177303 |
| note="assembly_fragment" | 175865. 177303 |
| note="assembly_fragment" | 17404. 179097 |
| note="assembly_fragment" | 179198. 181636
               165789. .169698
/note="assembly_fragment"
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Anote-"assembly_fragment"
19678 ...10659
10068 ...110659
110760 ...115413
Anote-"assembly_fragment clone_end:SP6 vector_side:right"
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note="assembly_fragment clone_end:T7 vector_side:left"
.56499. .161724
87441 87540: gap of 100 bp 87541 99577: contig of 12037 bp in length 99578 99677: gap of 100 bp 99578 110659: contig of 100 bp 110660 110759: gap of 100 bp 110760 115513: contig of 4654 bp in length 115513: gap of 100 bp 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115514 115
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/note="assembly_fragment"
5953. 74496
/note="assembly_fragment"
74597. 87440
/note="assembly_fragment"
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note="assembly_fragment"
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146073. .153170

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161825. .165688
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note="assembly_fragment"
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/db_xref="taxon:9606"
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/clone="RP11-879N20"
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1. .186351
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PAT 10-JUN-1998

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1 (bases 1 to 1425)
Sprecher.C.A.
Cytoplasmic antiproteinase-2 and cytoplasmic antiproteinase-3 and coding sequences
Patent: US 5710026-A 1 20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 GAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCGGCGGCGGCGGCGGCGCCAGCAG 392
                                                                                     Score 73.4; DB 6; Length 1425; Pred. No. 3.2e-07; 0; Mismatches 1; Indels 0
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                           Score 73.4; DB 6; Length 1425; Pred. No. 3.2e-07;
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Sprecher.C.A.
Cytoplasmic antiproteinase-2 and coding sequences
Patent: US 5712117-A 1 27-JAN-1998;
Location/Qualifiers
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                                                        0; Mismatches
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Sequence I from patent US 5712117.
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182208.1 GI:3210505
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Sequence 1 from patent US 5710026.
181228
181228.1 GI:3209518
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301 c 357 g
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Local Similarity 98.7%;
les 74; Conservative (
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Patent: US 5747645-A 1 05-MAY-1998;
                                                                                                                                                                                                                                                                                                                       8056 CTAAAATACGTAAAAAAAAAAAAAAAAAAAACCAAAACCAAAATCAAAACGAAAACAAA 7997
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                                                                                                                                                                                                                                               TGGAGTCAAACGTGAATCAACGGTGAAAAAGGACAATAGCCAATGTGTACACTTTTTAT 180
                                                                                                                                                                                                                                                                                                      181 AAAAACCACCTCCAAGGACCAGGCACTGGCCCTCTCTCCGGTGCCCACAGACATCCACA 240
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                                                                                                                                                                                       TGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 120
            /note="chemically treated genomic DNA (Homo sapiens)" a 187 c 2851 g 6180 t
                                                                                                 0; Gaps
                                                                                                                              1 GCCAACAAACAAAATGAAATAAGACCTGGGATGTATTTTTGGCCAAGGCAATTAGAAAA 60
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                                                                    Length 13202;
                                                                   Score 367.8; DB 5; Length :
Pred. No. 1.2e-78;
1; Mismatches 181; Indels
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Sequence 1 from patent US 5747645.
AR005195
/db_xref="taxon:32630"
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                                                                    Query Match 56.1%;
Best Local Similarity 72.3%;
Matches 474; Conservative
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Unclassified.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [ (bases 1 to 113684)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 GCGGCGGCGGCGGCGGCGGCAGCAGCAGCAGCAGGAGGTGGGGGGCCTCTGCCAGGTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 CCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 CCGGGCGGGCCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTGGAGT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 AAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGAAG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 GCGTGAGAGAGGGGAAGGAAGGCCAGAGAATCAGAGCGGAGGCAAAGGCGGGC
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                                                                                                            linear
                                                                                                                                                                                                                                                               Dorner, F., Scheiflinger, F. and Falkner, F. Gunter. Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                       1218 bp I Sequence 14 from patent US 5670367.
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HTG; HTGS_PHASE1.
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DFKEYCQKFYQAELEELSFAEDTEECRKHINDWVAEKTEGKISEVLDAGTVDPLTKLV
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YDLEPFLERLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEVNEEGTEAAAATAV
VRNSRCSRMEPRFCADHPFLFFIRRHKTNCILFCGRFSSP"
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                                                                                                                                                                                                                                                                                                                                                                                                         Sprecher, C.A., Morgenstern, K.A., Mathewes, S., Dahlen, J.R., Schrader, S.K., Foster, D.C. and Kisiel, W. Molecular cloning, expression, and partial characterization of two
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1325)
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Homo sapiens cytoplasmic antiproteinase 2 (CAP2) mRNA, complete
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333 GAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
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/note="(vector lambda gt11)"
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ilarity 100.0%; Pred. No. 4e-
Conservative 0; Mismatches
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/db_xref="taxon:9606"
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces
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Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 113684)
Norley.K.C.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. contig of 1049 bp in length gap of unknown length contig of 1150 bp in length contig of 1614 bp in length gap of unknown length gap of unknown length contig of 1016 bp in length gap of unknown length bp in length
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, Y., Boyuslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, Y., Boyuslavkiy, L., Anderson, S., Erwan, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Farreira, P., Kamat, A., Karatas, A., Kalls, G., Lakocque, K., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacChan, P., MacDanid, P., Major, J., Marquis, N., Matthews, C., MacChan, P., Madonald, P., Major, J., Marquis, N., Matthews, C., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retfa, R., Raback, M., Santos, R., Schauer, S., Schupback, R., Seaman, J., Rosetti, M., Pepenson, R., Palanas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viell, R., Anders, L., Tender, S., Theodore, J., Viell, R., Lander, J., Roman, S., Seweiy, P., Spencer, B., Stange-Thomann, N., Yughon, C., Rette, R., Landers, M., Travis, N., Travis, N., Vassiliev, H., Viell, R., Anders, A., Reile, R., Way, A., Willson, B., Wu, X., Wyman, D., Ye, W., Villson, B., Wu, X., Wyman, D., Ye, W., Ye, W., Zhan, C., Chan, R., Reile, A., A., Wallson, B., Wu, X., Wyman, D., Ye, W., Yillson, B., Wu, X., Willer, A., A., Wallson, B., Wu, X., Wyman, D., Ye, W., Ye, C., Chan, R., A., A., Wallson, B., Wu, X., Willer, A., A., Wallson, B., Wa, X., Wallson, B., Wa, X., Wallson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-AGG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 13, 2002 this sequence version replaced gi:20128326.
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                         Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-133N21
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generated and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1416 14275: gap of 100 bp 14276 15030: contig of 755 bp in length 15031 15130: gap of 100 bp 15131 15554: contig of 724 bp in length 15855 15954: gap of 100 bp 16689 in gap of 100 bp 16789: gap of 100 bp 17529: contig of 741 bp in length 17530 17629: gap of 100 bp 17530 18368 18367: contig of 788 bp in length 18368 18467: gap of 100 bp 18368 19221: contig of 784 bp in length 18467: gap of 100 bp 18368 19221: contig of 784 bp in length
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20072: contig of 751 bp in length
20172: gap of 100 bp
20911: contig of 739 bp in length
21011: gap of 100 bp
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21763: contig of 752 bp in length
863: gap of 100 bp
22609: contig of 746 bp in length
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23475: contig of 766 bp in length
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34435: contig of 740 bp in length

3535: gap of 100 bp

35357: contig of 722 bp in length

35357: gap of 100 bp

35314: contig of 757 bp in length
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47924: contig of 735 bp in length
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745 bp in length
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37: gap of 1
42857: contig of
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Search completed: January 10, 2003, 00:16:31 Job time: 2751.88 secs

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Human chromosome 18q; mood disorder; polymorphic marker; detection; identification; trinucleotide repeat expansion; schizophrenia; anxiety disorder; adjustment disorder; personality disorder; nucleotide triplet repeat; ss.
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Van Broeckhoven C;

Raeymaekers P,

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WPI; 1999-418934/35.

Epstein Barr virus

Fri

Detecting nucleotide triplet repeats in human chromosome 18q

Claim 21; Fig 15a; 87pp; English.

The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymozphic markers D18668 and D185979 to identify a human gene associated with a mood disorder or related disorder. AxX88542 to AxX88705 represents human chromosome 18q TAC clones and primers corresponding to them, used in the exemplification of the present invention. TAC clones comprising a portion of the region of human chromosome 18q between markers D18588 and plassypy are used to identify at least one human gene associated with a mood disorder. is chosen from the Diagnostic and Statistical Manual of Mental disorders, version 4 (DSM-TV) taxonomy. This includes mood disorders (206.xx, 300.44, 311, 301, 13, 297.30, Schizophrenia and related disorders (309.81, 308.3), adjustment disorders (309.XX) and personality disorders (codes 301.XX). Probes derived from genes associated with the mood disorder or related disorder can be used to detect pathological autitations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual conditions are used to determine and related disorder or related disorder. The nool disorders and the human gene can be used to treat mood disorders and related and personality of an individual

Sequence 656 BP; 183 A; 165 C; 208 G; 96 T; 4 other;

TGATTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAG 120 TGATTACTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACTAC 120 TGGAGTCAAACGTGAATCAACGGTGAAAAAGGACAATAGCCAATGTGTACACTTTTTAT 180 Gaps 1 GCCAACAAACAAATGAAATAAGACCTGGGATGTATTTTTGGCCAAGGCAATTAGAAAA 60 ö 99.5%; Score 652.6; DB 20; Length 656; 100.0%; Pred. No. 3.3e-155; ive 0; Mismatches 0; Indels 0; Conservative al Similarity 656; Conserv Query Match Best Local Matches 65 61 61 121 셤 δā g 9 $\delta \Delta$

121 g

AAAAACCACCTCCAAGGACCAGGCACTGGCCCTCTCCGGTGCCCCACAGACATCCACA 240 CAGGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTG 300 181 241 181 g $Q_{\overline{Q}}$ ŏ

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541 GGCGGCCAGGAACTANGAGAATGACSGCGGGGGGGGGCGGGAAAGAAANTCTCGGGGCT 600 900 GGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCT 541 d ŏ

601 GIGGGGGICNCCCIGGCACCAGCCGGGGICCCAAGCCCCAACGCGGAACCCCGGA 656

δ

656 601 g

Human; immune system disease; cytosine methylation; antiasthmatic; Human immune system associated gene SEQ ID NO: 1457. ABL33484 standard; DNA; 13202'BP (first entry) 26-MAR-2002 ABL33484; RESULT 2 ABL33484 品数

antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthitic; antidabetic; antipsoriatic; antirheumatory; cancer; eye disease; arteriosclerosis; anamaic; acute myeloid leukaemia; Alzheimer's disease, AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds.

Homo sapiens

WOZ00200928-A2.

03-JAN-2002.

02-JUL-2001; 2001WO-EP07537.

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30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.

(EPIG-) EPIGENOMICS AG

Berlin Olek A, Piepenbrock C,

ž

WPI; 2002-130909/17.

useful Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation

Claim 1; SEQ ID NO 1457; 32pp + Sequence Listing; German.

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulocrative bowel diseases. The present sequence is a gene of the invention.

Sequence 13202 BP; 3470 A; 187 C; 2897 G; 6648 T; 0 other;

Gaps DB 24; Length 13202; ; 0 Indels Score 441.6; DB 24; Pred. No. 1.9e-101; 1; Mismatches 133; 67.3%; Conservative Local Similarity es 519; Conserv Query Match Matches

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4670 AATAAATAAAATAAGATTAGGGATGTATTTTTTTGGTTAAGGTAAATAGAAAAGA 4729 4 AACAAACAAATGAAATAAGACCTGGGATGTATTTTTTGGCCAAGGCAATTAGAAATGA ď g

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TTAGTATCCTTATCAGGAGCAATTTCAGAGAATGTTTGGGTGGACGTCTAACTACAGTGG 123

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4849 124 AGTCAAACGTGAATCAACGGTGAAAAAGGACAATAGCCAATGTGTACACTTTTTATAAA 4790 셤 ŏ

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/alcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                               8416 TAAAATCAAACGTAAATCAACGATAAAAAAAAAAACCAATAATATATACACTTTTTAT 8357
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                                                                                                                                                                                                                                                                                              Length 13202;
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                                                                                                                                                                                                                                                 Sequence 13202 BP; 3984 A; 187 C; 2851 G; 6180 T; 0 other;
                                                                                                                                                                                                                                                                                           Score 367.8; DB 24; Length
Pred. No. 8.5e-83;
.; Mismatches 181; Indels
Claim 1; SEQ ID NO 1458; 32pp + Sequence Listing; German
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Best Local Similarity 72.3%;
Matches 474; Conservative
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QY
                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTAGCGGCGCGCGCGCGCGCTAGTAGTAGTAGTAGGAGGTGGCGCGTTTTTGTTA 5089
                                                                                                                                                                                 GAAGCCTTGCCCTCAATCAAGGGGGACGTGAAGCATCTACAAAGGAGAATAGTCAAAGC 363
                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                  GGTACCGGGCGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCAGGAACTANGAGAATGACSGCGGGAGGCGCCGGGAAAAAAATCTCGGGGCTGTG 603
184 AACCACCTCCAAGGACCAGGCACTGGCCCTCTCTCCGGTGCCCACAGACATCCACACAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, immune system disease; cytosine methylation, antiasthmatic; antiatrefisoslerotic; antianaemic; cytostatic; nootropic; neuroprotective; antianiento; cytostatic; obthalmologici; neuroprotective; antiarthritic; antidabetic; antipsoriatic; antishlammatory; cancer; eye disease; arterioscalorosis; anaemia; acute myeloid leukaemia; Alloshimer's disease; Allos; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                            4850 AATTATTTTAAGGATTAGGTATTGGTTTTTTTTTCGGTGTTTATAGATATTTATAG
                                                                                                                                                                                                         GCCCAAAGAATCAGGGATTGCACAAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCG
                                                                                                                                                                                                                                                                         AGCAGCGGCGGCGGCGGCGCCAGCAGCAGCAGCAGGAGGTGGGGGCCCTCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTGCGTGAGAGGGGAAGGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGTCNCCCTGGCACCAGCCGGGGTCCCAAGCCCCACCGCGAGACCCCGCGA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL33485/c
ID ABL33485 standard; DNA; 13202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÅĞ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17
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26-MAR-2002

8237

240

8177

8057

480

540

7937

900

Homo sapiens

dene;

30-JUN-2000; 01-SEP-2000;

Olek A,

03-JAN-2002

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333 GAAGCAICIACAAAGGAGGAGIATAGICAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                  A cDNA clone (AAT35220) codes for cytoplasmic antiproteinase-2 protein (CAP-2) (AAR99253), an inhibitor of specific trypsin-like serine proteases. It was isolated from a human placenta lambda still cDNA library by screening with a probe generated by PCR amplification of placenta cDNA using primers (see also AAT35222-23) hased on the CAP-1 protein. A cDNA clone (AAT35221) for CAP-3 (AAR99254) was also isolated. These cDNA clones can be incorporated into expression vectors and used for prodn. of recombinant CAPs in transformed or transfected host (pref. mammalian) cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caspase; serpin; inflammation; apoptosis; lung disease; human; CAP; neurodegenerative disease; heart; liver tissue; Alzheimer's disease; parkinson's disease; amyotrophic lateral sclerosis; injury; trauma; hypoxy ischaemia; cytoplasmic antiproteinase-2 protein; CAP-2; nootropic; neuroprotective; vasotropic; tranquilizer; vulnery; ss.
                                                                                                                                                                                                                                                                                                          Human cytoplasmic antiproteinase-2 (CAP-2) and CAP-3 - serine protease inhibitors useful in the purification of proteins and in the treatment of inflammatory diseases and apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytoplasmic antiproteinase-2 protein (CAP-2) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 73.4; DB 17; Length 1425; 98.7%; Pred. No. 9.5e-09; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1425 BP; 438 A; 300 C; 357 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 35-37; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ39749 standard; cDNA; 1425 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0072275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US08949.
                                                                              96WO-US01288.
                                                                                                                      95US-0385500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Conservative
                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 CAGCAGCAGCAGGAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 CAGCAGCAGCAGGAG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS.
                                                                                                                                                                                                                                                 WPI; 1996-393014/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                       P-PSDB; AAR99253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1998;
WO9624650-A2
                                                                                 02-FEB-1996;
                                                                                                                        08-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1999.
                                                                                                                                                                                                           Sprecher CA;
                                     15-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ39749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from cligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 ATCTGCCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAATA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic antiproteinase-2 protein; CAP-2; serpin; serine protease inhibitor; antiinflammatory; apoptosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 186 BP; 52 A; 43 C; 57 G; 34 T; 0 other;
                                                                                                                                                                                                                                                                                               Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%; Score 100; DB 21
99.1%; Pred. No. 9e-16;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 18069; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic antiproteinase-2 protein cDNA.
  gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 92..1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT35220 standard; cDNA; 1425
                                                                                                                                                                    21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                           99US-0122487.
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Matches 111; Conservative
                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
                                                                                                                                                                                                                                                     (GEST ) GENSET
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                                                                                   EP1033401-A2.
                                              Homo sapiens
                                                                                                                            06-SEP-2000.
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level in an unactivated the expression level in an unactivated of CG. where differential expression of Gs is indicative of GGA.

Also included are modulating (M2) GA by contacting of with an agent chart alters the expression of at least one gene in GS; (2) screening (M3) chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting the chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue where the exposure of a subject to a pathogen or sterile of inflammation with an agent that modulates the expression of gene(s) from GS in the tissue, where caponse in a subject, exposure of a subject to a pathogen or sterile inflammation fergerially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation injury, ARDS, adult respiratory distress syndrome, creptorile injury, ARDS, adult respiratory distress syndrome, periodontal disease; also bacterial infection, viral infection injury, and the sequence data for the law of the present sequence tepresents agene differentially defined in the present of 
                                                                  Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 AGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGCGCAGCAGCAGCA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCATCTACAAAGGAGGAGGAATAGTCAAAAGCAGCGGCGGCGGCGGCGGCGGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose synthase; cellulose production; increase yield; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1325 BP; 378 A; 286 C; 342 G; 319 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.1%; Score 73; DB 24; I 100.0%; Pred. No. 1.2e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                        Claim 1; SEQ ID No 465; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA10594 standard; DNA; 10732 BP.
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ses 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 GCAGCAGCAGGAG 407
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                         WPI; 2002-435328/46.
                                                                                                                                               drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA10594;
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AAA10594
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ZXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                           The invention provides a method for treating a disease mediated by a caspase in an individual. The method comprises: administering a composition comprising a gene coding for an intracellular mammalian serpin in an amount sufficient to inhibit activity of the caspase upon transient expression of the gene in a target tissue affected by the disease, where the disease or the symptoms are treated. The method can be used for decreasing inflammation, for modulating apoptosis, for treating a lung disease, and for treating a neurodegenerative disease. The inflammation and apoptosis that can be treated are particularly in heart or liver tissue. It can be used for treating Alzheimer's disease, parkinson's disease, amyotrophic lateral sclerosis, and acute injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as hypoxy-ischaemia or trauma. The present sequence represents a cDNA encoding the human cytoplasmic antiproteinase-2 protein (CAP-2), an intracellular serpin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for treating disease or symptoms of a disease mediated by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, ss, granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozcal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA differentially expressed in granulocytic cells #465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 11.2%; Score 73.4; DB 21; Length 1425; Local Similarity 98.7%; Pred. No. 9.5e-09; Local Stantive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1425 BP; 437 A; 301 C; 357 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beazer-Barclay Y, Weissman SM, Yamaga S,
                         Jaspers SR;
                                                                                                                                                                                                                Example 1; Page 55-56; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK83894 standard; cDNA; 1325 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2001; 2001WO-US30821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                    Sprecher CA, Foster DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 CAGCAGCAGGAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 CAGCAGCAGCAGGAG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC INC.
                                                                  WPI; 2000-062146/05.
P-PSDB; AAX55840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200228999-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                    caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK83894
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of
                                                                                                                                                                                                                            This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8867 ASTYRGGNYSTHRTRTRARGYSYSSRSRGYSTHRAAAAASASNTHRASTHRSRYSGASNG 8926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9044
                                                                                                                                                                                                                                                                                                                                                                                                                                                              325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 GCAGCAGCAGCAGCAGCAGGAGGIGGGGGCCTCTGCCAGGTACCGGGCGGGGCAGGCACG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCCGGGAGGCGGCCGGGAAAGAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCG 625
                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGGCCCTCTCTCCGGTGCCCACAGACATCCACACGGCCCAAAGAATCAGGGATTGCA 265
                                                                                                                                                                         gene encoding a cellulose synthetic equipment - for the improvement n the amount of cellulose synthesised in a plant body
                                                                                                                                                                                                                                                                                                                                                                        146 AAAAAAGGACAATAGCCAATGTGTACACTTTTTATAAAAACCACCCTCCAAGGACCAGGC 205
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAAAGGCGGGCAGGAACTANGAGAATGAC
                                                                                                                                                                                                                                                                                                                              7.7%; Score 50.4; DB 21; Length 10732; 21.8%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                         Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
                                                                                                                                                                                                                                                                                                                                                    Matches 111; Conservative 152; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGICCCAAGCCCCACGCGAGACCCCGC 654
                                                                                                                                                                                                         Claim 2; Page 14-21; 32pp; Japanese
                                                              98JP-0239998
                                                                                     98JP-0239998
                                                                                                         (MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO.
                                                                                                                                         WPI; 2000-342371/30.
P-PSDB; AAY85179.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
Vigna angularis.
                    JP2000060568-A.
                                                               86-AUG-1998;
                                                                                     26-AUG-1998;
                                          29-FEB-2000.
                                                                                                                                                                                                                                                                                                                                 Query Match
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This DNA encodes a stabilising polypeptide and is the FLGA insert of the invention. The invention provides a method for increasing the resistance of a core protein to proteintyle degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula [(Glya)X(Glyb)X(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential [Glya)X(Glyb)X(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr and n can be anything between 1-66 X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein. The products can be used for treating autolimmune disease, cancer and inflammatton. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, on a nitroreductase protein treatment of inflammatory bowel disease, or a nitroreductase protein core protein pathological conditions. The fusion proteins can also be used in
                                                                                                                                                                                                                                                                   Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion proteins resistant to proteolytic degradation -
comprising a core protein with a stabilising polypeptide comprising
a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                                                                  nitroreductase protein; enzyme therapy; prodrug therapy; protease, cancer; pathological condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 0.0057;
0; Mismatches 146; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 795 BP; 200 A; 104 C; 478 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "stabilising polypeptide""
                                                                                                                                                                                                       FLGA insert stabilising polypeptide encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic methods such as in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 3; 120pp; English.
   BB
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nilarity 48.2%; Conservative 0,
AAV55830 standard; DNA; 795
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96US-0030986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product=
                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-312463/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW79128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09822577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Simi
les 136;
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                                                                                                                                     18-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                  AAV55830;
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                                                                                                                                                                                                                                                                                                           Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV orip: receptor: eucaryotic host cell; recombinant cell line; ion channel; gene therapy; multiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a DNA encoding Epstein Barr Virus Nuclear Antigen 1 (EBNA 1), which is obtained from commercially available plasmid pcMVEBNA. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (oriP) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a
                                                            526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAA 585
 406 AGGTGGGGGCCTCTGCCAGGTACCGGGCGGGCCAGGCACGGAGGTGCCCAGGTTCCCGCG 465
                                                                                                               /fransl_except= (pos:799..800, aa:Gly)
/note= "The sequence is described throughout the
specification as being 1926 nucleotides long, but a
sequence of only 1925 bp has been given in figure 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New method for expressing genes from recombinant eukaryotic cells,
                                               466 GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGAGGGGAAGGGAAGGCCAGAGGCAGGGAA
                                                                                                                                       586 GAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGG 627
                                                                                                                                                            GGGCAGGAGGCAGGAGCAGGGGCAGGAGCAGGAGGGGG 473
                                                                                                                                                                                                                                                                                         Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Damaj BB, Horlick RA, Robbins AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "EBNA 1"
                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                      AAX90924 standard; DNA; 1925
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98US-0130114.
                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                       cell immortalisation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610610/52.
P-PSDB; AAY28843.
                                                                                                                                                                                                                                                                                                                                                                                             Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9947647-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-1998;
                                                                                                                                                                                                                                                                   17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-1999
                                                                                                                                                                                                                                            AAX90924;
                                                                                                                                                                                                 RESULT 10
AAX90924
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rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors. transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
                                                                                                                                                                                                                                                                                                                                              406 AGGTGGGGGCCTCTGCCAGGTACCGGGCGGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 GAGGCCACCTTCCCTGGAGTGCGTGAGAGAGGGGAAGGGAGGAAGGCCAGAGCAAGGAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCGGGAAA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                      Score 49.2; DB 20; Length 1925;
Pred. No. 0.014;
1; Mismatches 120; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                       Sequence 1925 BP; 486 A; 352 C; 872 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #20895.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS85091 standard; cDNA; 3103
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                                                                                                                                                                                                                                           h
Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                               Matches 120;
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                                                                                                                                                                                                                                           Query Match
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymcleotides are also used in diagnostics as expressed sequence tags of the identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in itssue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 AGGIGGGGGCCTCTGCCAGGTACCGGGCGGGCAGGCACGGAGGTGCCCAGGTTCCCGCG 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 47.2; DB 23; Length 3103; Best Local Similarity 54.7%; Pred. No. 0.052; Matches 94; Conservative 0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Essioux
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3103 BP; 669 A; 871 C; 899 G; 664 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-IB01730.
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AAA55964
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polynucleotide (PM) (1) comprising a contiguous span of 8 to 50 nucleotides, where the span includes a G713 or chromosome 13431-q33 related hallelic marker. (1) has neuroleptic activity and can be used as a G713 gene expression inhibitor. (1) can be used genotyping to estimate the frequency of an allele of a G713 or chromosome 13431-q33 related biallelic marker in a population, and of a haplotype for a set of biallelic markers in a population. (1) is also useful in detecting an association between a haplotype and a trait. The frequency is used for detecting an association between a genotype and a trait being schizophrenia. The genotype is used to determine whether an individual is at risk of developing schizophrenia. (1) can also be used as a medicament against several disorders preferably brait, psychiatric clisorders such as schizophrenia and bipolar disorder. Early identification of risk of developing schizophrenia and bipolar disorder. Early identification of risk of developing schizophrenia (1) and also be used as a medicament as and/or prophylactic treatment. AAA55967 encodes the numan G713 protein AAY90962; AAA55968 encodes the murine G713 protein and AAA5603 represent human G713 protein and AAA5603 represent promarkers A12 to A43; AAA55961, and AAA56031 represent PCR primers used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 AGGIGGGGGCCICIGCCAGGIACCGGGGGGGGGGAGGCACGAGGIGCCCAGGIICCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                      The present invention describes an isolated, purified or recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia; biallelic marker; polymorphism; central nervous disease; detection; neuroleptic; G713 gene expression inhibitor; genotyping; brain disorder; psychiatric disorder; bipolar disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Length 5222;
prophylactic treatment of brain, psychiatric disorders like schizophrenia and bipolar disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5222 BP; 1278 A; 1304 C; 1439 G; 1176 T; 25 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.1%; Score 46.8; DB 21; Length Best Local Similarity 58.7%; Pred. No. 0.078; Indels
                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G713 encoding cDNA SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA55967 standard; cDNA; 5566 BP.
                                                          Page 211-212; 271pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4084 CACACAGACTCCTCCG 4101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0103955.
98US-0106457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
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AAQ95180 is a simple tandem repeat (STR) corresponding to wgla9. The STR can be used for treatment and diagnosis in himan and veteribary medicine, partic. for genetic obaracterisation, mapping, linkage studies and analysis/diagnosis of acquired disease alleles.
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detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                        Identifying simple tandem repeat loci in DNA - by screening DNA library to enrich for fragments contg. the repeats before cloning and rescreening, also simple tandem repeats for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46.4; DB 16; Length 286;
Pred. No. 0.037;
0; Mismatches 41; Indels 0.
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo P, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:4529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 TCTGCCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 286 BP; 74 A; 71 C; 81 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Claim 26; Page 18; 51pp; English.
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98US-0072910.
98US-0075954.
98US-0080114.
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                                                                93GB-0026052.
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                    94WO-GB02789
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                                                                                                            UYLE-) UNIV LEICESTER.
                                                                                                                                                     Armour J, Jeffreys AJ;
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                                                                                                                                                                                              WPI; 1995-240682/31.
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                    21-DEC-1994;
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31-MAR-1998;
                                                              21-DEC-1993;
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28-JAN-1998;
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                                                                                                                                                                                                                                                                                                          diagnosis
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Matches
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ID AAZ1
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                                                                                                                                                                                                                                                                        The present invention describes an isolated, purified or recombinant polynucleotide (PN) (I) comprising a contiguous span of 8 to 50 nucleotides, where the span includes a G713 or chromosome 13431-q33 crelated biallelic marker. (I) has neuroleptic activity and can be used as a G713 gene expression inhibitor. (I) can be used genotyping to estimate the frequency of an allele of a G713 or chromosome 13431-q33 crelated biallelic marker in a population. (I) is also useful in detecting an association between a haplotype and a trait. The frequency is used for detecting an association between a genotype and a trait being shizophrenia. The genotype is used to detecting an association between a genotype and a trait being schizophrenia. The genotype is used to determine whether an individual is at risk of developing schizophrenia. (I) can also be used as a medicament against several disorders preferably brain, psychiatric disorders such as schizophrenia and bipolar disorder. Early indentification of risk of developing schizophrenia is possible, which confidentification of risk of developing schizophrenia is possible, which the multing confidential pary9062; AAA55968 encodes the murine G713 protein AAY9062; AAA55967 encodes the human G713 protein AAY9065; AAA55967 encodes the human G713 protein AAX9065; AAA55967 encodes the human G713 protein AAX90651, and AAA56031 and AAA56032 represent PCR primers used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 AGGIGGGGCCICTGCCAGGIACCGGGCGGGGCAGGCACGAGGTGCCCAGGTTCCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simple tandem repeat; STR; wqla9; treatment; genetic; diagnosis; characterisation; mapping; linkage studies; analysis; alleles; ss
                                                                                                                                                     useful for diagnosis and
                                             Essioux L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%; Score 46.8; DB 21; Length 5566; 58.7%; Pred. No. 0.08; tive 0; Mismatches 57; Indels 0;
                                                                                                                                                                            prophylactic treatment of brain, psychiatric disorders like schizophrenia and bipolar disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5566 BP; 1605 A; 1187 C; 1299 G; 1466 T; 9 other;
                                           Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simple tandem repeat (STR) corresponding to wgla9.
                                           Chumakov I,
                                                                                                                                                     Novel polynucleotide of human G713 gene
                                                                                                                                                                                                                                            Claim 1; Page 231-233; 271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ95180 standard; DNA; 286 BP
                                             Blumenfeld M, Bougueleret L,
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                                                                                       WPI; 2000-317979/27.
                                                                                                              P-PSDB; AAY90962.
(GEST ) GENSET
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Query Match Local Matches

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Synthetic.

AAQ95180;

RESULT 14 AAQ95180

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Gaps

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Stache-Crain B, Sudduth-Klinger J, Williams II;

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Novel human genes and their expression products which are differentially expressed in different cell types

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Novel human genes and their expression products which are differentially expressed in different cell types

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Claim 1; Page 2147; 2479pp; English.

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XX

Camerhoo of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising derecting at least one differentially expressed gene product in a test sample from a cell cancerous state of a mammalian cell, comprising derecting at least one differentially expressed gene product in a test sample from a cell compressed of being cancerous, where the gene product is encoded by one of the 524B polyuucleotide sequences given in AAZ12532 to AAZ1779. The collyuucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of Polyuncholisms. Polypeptides encoded by the polyuncleotides for experimental, diagnostic and charapeutic purposes. The polyuncleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polyuncleotides of the invention are especially used in the dentify and analogues and management of colorectal cancer, breast cancer, and lung cancer. The polyuncleotides can also be used to screen for companied and antagonists.

X Sequence 1017 BP; 143 A; 117 C; 482 G; 21 T; 254 other;
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Sequence 1017 BP; 143 A; 117 C; 482 G; 21 T; 254 other;

Query Match 7.1%; Score 46.4; DB 20; Length 1017;

Best Local Similarity 42.3%; Pred. No. 0.056;

Matches 90; Conservative 0; Mismatches 123; Indels 0; Gaps

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OY 481 CIGGAGIGCGIGAGAGAGGGGAAAGGCCAGGAAGCCAGGAATCAGAGCGAAA 540

DD 662 GENGNGGERENGAGEGEGENAGEGGGGUNGAGCNGGGNNNNCAGGGUNGNANG 721

OY 541 GGCGGGCAGGAACTANGAGAATGACSGCGGGAG 573

722 GNGNNNAGGNGGCGNNGGGGAGGAGNGNGGGAG 754

Search completed: January 9, 2003, 21:33:45 Job time: 327.247 secs

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Sequence 13, Appl
Patent No. 5196516
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                                     Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 3, A Sequence 3, A Sequence 1, Sequence 60, Sequence 60,
                                                                                                                         1, 1
60,
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Sequence 3, 7
Sequence 2, 7
Sequence 12,
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               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER EALDALE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC COMPATIBLE
COMPOTER: TBM PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,148
FILING DATE: OS-UN-1995
PRICA PAPLICATION NUMBER: US 08/385,500
FILING DATE: O8-FEB-1995
ATTORNEY/AGENT INFORMATION:
ANNUM DESCRIPTION: ANNUMBER: OS-PEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie and Crew STREPT: Steuart Street Tower, One Market Plaza CITY: San Erancisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /product= "CYTOPLASMIC ): OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN" US-08-464-148-1
          US-08-455-0734-1

US-08-149-0970-22

US-08-450-562-22

US-08-450-562-22

US-08-450-562-22

US-08-09-070-816-3

US-09-070-816-3

US-09-135-994-3

US-09-146-249A-60

US-09-146-249A-60

US-09-146-249A-60

US-08-146-249A-60

US-08-146-249A-60

US-08-146-249A-1

US-08-146-14A-1

US-08-146-14A-1

US-09-146-14A-1

US-09-140-14A-1

US-09-140-14A-1

US-09-477-044B-3

US-09-477-044B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REPERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/08464148; Patent No. 5710026; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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LOCATION: 92..1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 94105-1493
STATE: CZ
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US-08-464-148-1
Query Match
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3642.332 Million cell updates/sec
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                                                                                            January 9, 2003, 21:50:31; Search time 55.2338 Seconds
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Sequence 3,
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/ina/5A_COMB.seq:*/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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US-08-38-500-1

US-08-23-463-14

US-09-009-816-1

US-09-009-816-1

US-08-23-766A-6

US-09-041-86-20

US-09-179-801-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-5

US-09-298-441-1

US-09-298-20-35-1

US-09-29-25-1

US-09-130-114-1

US-09-620-925-1

US-09-620-925-1

US-09-620-925-1

US-09-620-925-1

US-08-081-15-15

US-08-08-11-15

US-08-08-11-15
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US-08-458-745-1
US-08-406-030A-3
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                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   - nucleic search, using sw model
                                                                                                                                                                                                        IDENTITY_NUC Gaport 1.0
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Maximum DB seq length: 200000000
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656
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Match Length
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393 CAGCAGCAGCAGGAG 407
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                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 94105-1493
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                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08385500
Patent No. 5712117
GENERAL INFORMATION:
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 GAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 GAAGCATCIACAAAGGAGGAATAGICAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCAGCAG 392
                       Gaps
                                                                                          7 GGAGCATCTACAAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGC 66
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Pred. No. 1.6e-10;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
MEDIOW TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERCEATING PC-DOS/MS-DOS
SOFTWARE: PERCEATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US/08/385,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 92..1213
CTHER INFORMATION: /product= "CYTOPLASMIC; OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
US-08-385-500-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Parimelee, Steven W.
REGISTRATION NUMBER: 31,990
REFRENCE/DOCKET NUMBER: 31,990
TELEPRONE (206) 467-9600
TELEPRONE: (206) 467-9600
TELEPRONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
ENGURNE CHARACTERISTICS:
LENGTH: 1425 base pairs
98.7%;
Best Local Similarity 98.79
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 CAGCAGCAGCAGGAG 407
                                                                                                                                                           393 CAGCAGCAGCAGGAG 407
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-846-784-1
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US-08-385-500-1
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Sequence 1, Application US/08846784
Patent No. 5747645
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESTONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 GAAGCATCTACAAAGGAGGAATAGTCAAAAGCAGCGGCGGCGGCGGCGGCGGCAGCAG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: TBM FC Competition
COMPUTER: TBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION NUMBER: US/08/846,784
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATMELE & STEW-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATME
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CHERELINGER, F.
APPLICANT: SCHERFLINGER, F.
APPLICANT: FALKNER, F. G.
TILLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
WUMBER OF SEQUENCES: 52
CORRESPONDENCE: ADDRESS:
ADDRESSEE: FOLLY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 92..1213
CTHER INFORMATION: /product= "CYTOPLASMIC;
OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
US-08-846-784-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-232-463-14/C
Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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481 CTGGAGTGCGTGAGAGAGGGGAAGGGAGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 CCAGGTACCGGGGGGGGGGAGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 CAGGATATTGTTGATGCCGTGTGGGGTGGCGGCCGAGAGCTGCTGCGGGGGGGCTGCCGAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.5%; Score 49.4; DB 4; Length 1104; Best Local Similarity 50.9%; Pred. No. 0.00041; Matches 113; Conservative 1; Mismatches 108; Indels 0
            APPLICANT: German, Michael
APPLICANT: Permutt, M. Alan
APPLICANT: Permutt, M. Alan
APPLICANT: Inoue, Hiroshi
TITLE OF INVENTION: Human NKx-6.1 Polypeptide-Encoding
TITLE OF INVENTION: Nucleotide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITT: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 GGATGAGGCCCCCCGTGGCCGGGGGCTTCAGGCCGCTGG 205
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                                                                                                                                                                                                                                                                                                   SOUTWARE: PastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00 ^^^ CLACETING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9076/082CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-332-766A-6; Sequence 6, Application US/08332766A; Patent No. 5843647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 9076,
TELECOMMUNICATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYETM: DOS
SOFTWARE: FastSEQ for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAME/KEY: Coding Sequence CCATION: 1...1101 CTHER INFORMATION: US-09-009-816-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1104 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-327-3231
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TOPOLOGY: linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                94301
                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 CCTTGCCCTCAATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAAGAATAGTCAAAAGCAGCA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 GCGGCGGCGCGCGCGCGCAGCAGCAGCAGCAGCAGGAGGTGGGGGCCTCTGCCAGGTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 CCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTGGAGT 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 AAAGAATCAGGGATTGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGAAG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 3.8%; Pred. No. 7.6e-10;
Matches 15; Conservative 234; Mismatches 142; Indels
                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608 TCNCCCTGGCACCAGCCGGGTCCCAAGCCC 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09009816 Patent No. 6436667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)836-9300
(703)683-4109
                                      COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; CLONE: pTZgpt-Fls
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
Alexandria
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US-09-009-816-1/c
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PatentIn Release #1.0, Version #1.25
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STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
FILING DATE: January 7, 1997
                                                                                                                                                                            P-LJ 2626
               CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
RETERROCACOCKET NUMBER: P-LO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3563 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.5
Matches 139; Conservative
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                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Texas
                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
US-09-041-886-20
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-779-801-5
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 TCCTGGGATAACTCAGGTGAGTAGAGAGGGAATTCGCAAACTTACCCTGGAG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 46.4; DB 2; Length 286; 63.4%; Pred. No. 0.0015; tive 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                  COMPUTE: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
CLASSIFICATION 1994
CLASSIFICATION A35
PRIOR APPLICATION A35
PRIOR PEPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRAFION NUMBER: 25,323
NUMBER: OF A 124 AGENTALION NUMBER: 2,323
NUMBER: OF A 124 AGENTALION NUMBER: 25,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB TELEOROMAUNICATION HORDAMATION: TELEPHONE: (202) 861-3000 TELEPAX: (202) 822-0944 TELERAX: (314627 QGSH4 INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
               TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
CORRESCEE: CUSHMAN DRRBY & CUSHMAN, L.L.P.
                                                                                                   STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09041886
Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California COUNTRY: United States ZIP: 92122
                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 286 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.44
Matches 71; Conservative
APPLICANT: ARMOUR, John
                                                                                                                                                                                         ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                              STATE: D. C. COUNTRY: U.S.A. ZIP: 20005-3918
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US-09-041-886-20
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Sequence 5, Application US/08779801
Patent No. 585395
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
TITLE OF INVENTION: Diseases and a Diagnostic Test for Spinocerebellar Ataxia '
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               3066 GCCGAGCCTCTGGCCGGAGATCGGCCGCCCACGGGGGGCCACAGCAGCGCCGCCGCTCGCCC 3125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3126 adgarggagagggggroccaggcccggagcgagagccccagggccrgrcarca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 ATCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAA 584
                                                                                                                                                                                                                                                                                                                                                                 3186 GGCGGGGCCCGGTGTCTGCGACGGGCCCCCGGGTCCCCG 3244
                                                                                                                       405 GAGGTGGGGGCCTCTGCCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGC 464
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                                                                  Gaps
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7.0%; Score 46; DB 4; Length 3563; 46.5%; Pred. No. 0.0057; tive 1; Mismatches 159; Indels
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3066 GCCGAGCCTCTGGCCGGAGATCGGCCGCCCACGGGGGGCCACAGCAGCGGCCGCTCGCCC 3125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 7.0%; Score 46; DB 4; Length 3596; Best Local Similarity 46.5%; Pred. No. 0.0057; Matches 139; Conservative 1; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-1779-801-3
Sequence 3, Application US/08779801
Patent No. 5853995
GENERAL INSTALTION:
THILE OF INVENTION: Large Scale Genotyping of
                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
RESISTRATION NUMBER: 35,423
REFERRINGE/DOCKET NUMBER: D5968D/C
TELECOMMUNICATION INFORMATION:
                                                                                                        SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primary human brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3596 basepairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                  COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: BI-1(V2)-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (713) 777-2321
TELEPAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                          E: Floppy disk
Apple Macintosh
                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE:
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
US-09-298-441-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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Patent No. 6303307

GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of Diseases
TITLE OF INVENTION: and a Diagnostic Test for Spinocerebellar Ataxia Type 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 GAGGTGGGGGCCTCTGCCAGGTACCGGGCGGGGCAGGCACGGAGGTGCCCAGGTTCCCGC 464
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Pred. No. 0.0057;
1; Mismatches 159; Indels
                                                                                                          NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: primary human brain cDNA CLONE: BI-1(V2)-GGCAG POSTION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                    TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 46.5%;
Matches 139; Conservative
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                                                                                       ATTORNEY/AGENT INFORMATION:
                     PRIOR APPLICATION DATA:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brain
                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human
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STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11:
                                                                                                                                                                                                                                                                                              LENGTH: 3596
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: ht
                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
US-08-779-801-5
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Sequence 3, Application US/09298441

Patent No. 6303307

GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: and a Diagnostic Test for Spinocerebellar Ataxia Type 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968D/C
TELECOMMUNICATION INFORMATION:
TELEPAN: (713) 777-2321
TELEPAN: (713) 777-2321
TELEPAN: (713) 777-6308
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SISTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: primary human brain cDNA CLONE: BI-1-GGCAG POSITION IN GENOME:
                                                                                                                                                                                                                                          E: McGregor & Adler, LLP
8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 3632 basepairs
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ou
                                                                                                                                                                                                                                                              STREET: 8011 Ca
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
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Best Local Simi
Matches 139;
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Diseases and a Diagnostic Test for Spinocerebellar Ataxia Type
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3222 GGCGGGGCCCGGTGTGGGCGGCACGTCTGGAGGGGCCCCGGGGTCCCCG 3280
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46.5%; Pred. No. 0.0057;
tive 1; Mismatches 159; Indels
                                                                   ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D. STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/TOKET NUMBER: D5968
TELEBOMMUNICATION INFORMATION:
TELEBOMMUNICATION INFORMATION:
TELEBOMMUNICATION INFORMATION:
TELEBOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/779,801
FILING DATE: January 7, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: primary human brain cDNA CLONE: Br.1-GCGAG POSITION IN GENOME: CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.5
Matches 139; Conservative
                                                                                                                                                                                                      COMPUTER READABLE FORM:
  TITLE OF INVENTION: Di
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: CDNA
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TISSUE TYPE: bra
IMMEDIATE SOURCE:
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                                                                                                                Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3632
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                                                                                                                                                             USA
                                                                                                                                       STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
ANTI-SENSE: no
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-779-801-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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526 TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAA 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGCAAGGCCAGAGCAGGAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

PEPLICAMY: HOTLICK, RODERT
TILLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REPERENCE: 0867/0905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT APPLICATION NUMBER: 1999-02-11
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN PERSON 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.4; DB 4; Length 1926;
Pred. No. 0.0063;
1; Mismatches 145; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                586 GAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09050863
Patent No. 6114111
GAREAL INFORMATION:
GARLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF ENFORMENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS

LOCATION: (1)...(1926)

OTHER INFORMATION: coding strand of EBNA-1 DNA

US-09-249-588A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/09249585A Patent No. 6417002
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.98;
                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 142; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4 Embarcade)
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IJ
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                                                                                                                                                                                                                                           LENGTH: 1926
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US-09-050-863-2
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    162 AGGATGGAGAGGGGGTCCCAGGCCCGGAGCAACTCCCCCAGGGCCTGTCGACAC 3221
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                                                                                           3222 GGCGGGGCCGGGTGCCGGCACCTGCCCGACGTGCCCGGGGGCCCCCGGGTCCCCG 3280
                                                                     585 AGAAANTCICGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCCAAGCCCCACCG
                                                                                                                                                                                                                  Sequence 3, Application US/08531927B
Patent No. 5840491
GENERAL INFORMATION:
APPLICANT: Kakizuka, Akira
APPLICANT: Kakizuka, Akira
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
WUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 45.8; DB 2; Length 325; illarity 69.4%; Pred. No. 0.0023; Conservative 2; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/531,927B
FILING DATE: 21.5EP-1995
CLASSIFICATION: 435
PRIOR APPLICATION NOMBER: JP H6-251600
FILING DATE: 21.5ER-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 GCAGCAGCAGGAGGTGGGGGCC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 GCAGCAGCAGCAGCAGSGGGAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 59; Conserve
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US-08-531-927B-3
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US-09-249-585A-2
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US-08-531-927B-3
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Query Match Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGGGGGGCGGCGGGAAA 585
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Mammalian Protein Interaction Cloning System
                                                                                                                                                                                                                                                                                                                        6.9%; Score 45.4; DB 3; Length 2580;
49.0%; Pred. No. 0.0071;
Live 1; Mismatches 145; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586 GAAANTCTCGGGGGTGTGGGGGTCNCCCTGGCACCAGCCGGGTCCCAAG 635
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
               RECISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781.1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ILENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/050,863
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ATTORNEY/AGENT INFORMATION:
NAME: SILVA, RODIN M.
REGISTRATION WUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09359081 Patent No. 6316223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lao, Ying
Hiang, Betty
Payan, Don
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-4187
Silva, Robin M.
                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: DNA
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US-09-359-081-2
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526 TCAGAGCGAGGCGAAAGGCGGGCAGGAACTANGAGAATGACSGCGGGGGGGCGGCGGGAAA 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 GAGGCCACCTCTTCCCTGGAGTGCGTGAGAGAGGGGAAGGGCAGGAAGGCCAGAGAA
                                                                                                                                                                                                                                                                                                        6.9%; Score 45.4; DB 4; Length 2580;
49.0%; Pred. No. 0.0071;
tive 1; Mismatches 145; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 GAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGCCGGGGTCCCAAG 635
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  search completed: January 10, 2003, 06:37:32
Job time : 72.2338 secs
                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPEX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
                                                                                                                                                                      STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                     MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                    Local Similarity
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January 10, 2003, 01:01:36 ; Search time 85.8611 Seconds (Without alignments) 3362.497 Million cell updates/sec
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656
1 gccaacaaacaaatgaaat......cccaccgcgagaccccgcga 656
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| cgat_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgat_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgat_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgat_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgat_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgat_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgat_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgat_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389086 seqs, 220051671 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	Description	Sequence 94, Appl	Sequence 309, App	Sequence 1, Appli	Sequence 4, Appli	Sequence 7244, Ap	Seguence 8950, Ap	Sequence 37, Appl	Sequence 23975, A	Sequence 22135, A	Seguence 18923, A	Sequence 2182, Ap	Sequence 5361, Ap	Sequence 272, App	Sequence 14967, A	Sequence 1, Appli	Sequence 4578, Ap	Sequence 13, Appl	Sequence 15, Appl	Sequence 14, Appl
	ID	US-09-974-298-94	US-10-044-090-309	US-09-416-384A-1	US-09-416-384A-4	US-09-864-761-7244	US-09-864-761-8950	US-10-124-800-37	US-09-864-761-23975	US-09-864-761-22135	US-09-864-761-18923	US-09-864-761-2182	US-09-864-761-5361	US-09-925-297-272	US-09-960-352-14967	US-10-005-858-1	US-09-878-574-4578	US-09-849-243-13	US-09-849-243-15	US-09-849-243-14
	DB	σ	12	10	10	10	10	6	70	10	10	10	70	10	10	12	10	თ	σ	9
	Query Match Length DB	1476	2724	5222	5566	599	599	3886	230	210	293	459	464	527	311	2453	612	1310	3263	4286
æ	Query	14.0	7.3	7.1	7.1	7.0	7.0	6.9	6.8	6.7	6.7	6.3	6.7	9.9	6.5	6.5	6.5	6.4	6.4	6.4
	Score	91.8	47.8	46.8	46.8	45.6	45.6	45.4	44.8	44	44	44	44	43	42.8	42.6	42.4	42.2	42.2	42.2
	Result No.	Т	0	m	4	r)	9	0	8	σv	10	11	12	13	14	15	16	17	18	19

RESULT 2
US-10-044-090-309/c
; Sequence 309, Application US/10044090
; Patent No. US2020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman

Sequence 11, Appliance gequence 159, Applia Sequence 2300, Applia Sequence 2300, Applia Sequence 212, Applia Sequence 21, Applia Sequence 20, Applia Sequence 108, Applia Sequence 1097, Applia Sequence 1195, Applia Sequence 1185, Applia	:R :89880CB1	Length 1476; Indels 0; Gaps 0; Raangagagagagagagagagagagagagagagagagaga
9 US-10-078-650-11 9 US-10-078-650-1 10 US-09-728-445-159 10 US-09-980-107-2300 10 US-09-880-107-2300 10 US-09-861-761-8824 12 US-10-002-600-23 10 US-09-861-165-20 10 US-09-976-165-21 10 US-09-976-165-21 10 US-09-976-165-21 10 US-09-976-165-21 10 US-09-976-165-21 10 US-09-976-165-21 10 US-09-976-165-21 10 US-09-976-168-108 10 US-09-946-807-108 10 US-09-946-807-108 10 US-09-946-807-1097 10 US-09-975-668-1097 10 US-09-976-681-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097 10 US-09-795-668-1097	ALIGNMENTS US/09974298 AL SE EXPRESSED IN BREAST CANCERP BR: US/09/974,298 001-10-04 R: 60/238,331 05-10 94 YTE ID NO. US20020156263A1 58	tch al Similarity 93.2%; Pred, No. 4.6e-15; 96; Conservative 09; Mismatches 7; Indels 0; G CCCAATCAAGCGGGAGGAAAGCATCACAAAGGAGAAAAGAGAGAG
42 6.4 3641 41.6 6.3 2526 41.6 6.3 2526 41.4 6.3 2515 41.4 6.3 2515 41.4 6.3 122 41.2 6.3 1518 41.2 6.3 1518 41.2 6.3 1518 41.2 6.3 1518 41.6 5.2 1518 41.6 5.2 1518 41.6 5.2 1508 41.6 5.2 1508 40.8 6.2 1508 40.8 6.2 1508 40.8 6.2 1508 40.8 6.2 1508 40.6 6.2 1508	98-94 94, Application US 94, Application US 94, Application US 10, US2002015653A1 NRORMATON: TINCHANTION: GENES TINCHENTION: GENES TERRENCE: PREDENCE: PREDICATION NUMBER: FILING DATE: 2001 PRICATION NUMBER: TING DATE: 1100 DATE: 12000-05 15: PERL PROGRAM 1476 M: Homo sapiens M: Homo sapiens M: SE 18: S	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	RESULT 1 US-09-974-2 Sequence Retent Moderate 1 GENERAL 1 APPLICAN FILE REF FILE REF CURRENT CURRENT PRIOR PIP PRIOR PIP SOFTWARE	Query M Best Lo Bast Lo Matches QY 315 QY 375 Db 61

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RESULT 4

UG-90-416-384A-4

IG-90-416-384A-4

Sequence 4, Application US/09416384A

Sequence 4, Application US/09416384A

Sequence 4. Replication US/090168184AI

Sequence 4. Application US/090168184AI

Sequence 4. Application US/0901681AI

APPLICANT: BLUMENELD, Marta

APPLICANT: BOUGUELERET, Lydie

APPLICANT: GOHEN, Daniel

APPLICANT: GOHEN, Daniel

APPLICANT: GOHEN, Daniel

TITLE OF INVENTION: Genes, proteins and biallelic markers related to central...

FILE REPERENCE: GENEET 004508

CURRENT PLING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-30

PRIOR FILING DATE: 1999-10-30

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-30

PRIOR FILING DATE: 1999-0-0-03

SOFWWARE: Patent.pm

SEQ ID NO 4

SEQ ID NO 4

SEQ ID NO 4

SERVER PRIOR PATENT OF THE P
                                                                                    NAME/AEI TITLE

LOCATION: 3606

CTHER INFORMATION: insertion of AGAG in SEQID4

NAME/KEY: priner_bind

LOCAFION: 4572.4587

OTHER INFORMATION: 8-58.pu

NAME/KEY: priner_bind

LOCAFION: 4930.5005

OTHER INFORMATION: 8-58.pu

NAME/KEY: priner_binding

LOCAFION: 4849.4895

OTHER INFORMATION: 8-58-301.probe

NAME/KEY: priner_bind

LOCAFION: 4853.4871

OTHER INFORMATION: 8-58-301.mis

NAME/KEY: priner_bind

LOCAFION: 4873.4891

OTHER INFORMATION: 8-58-301.mis complement

LOCAFION: 4873.4891

OTHER INFORMATION: 8-58-301.mis complement

LOCAFION: 4873.4891

OTHER INFORMATION: 8-58-301.mis complement

NAME/KEY: misc_feature

LOCAFION: 148,686,902,1258,1322,2440,2794,2852,3018.3023,3054

US-09-416-384A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 AGGIGGGGCCTCTGCCAGGIACCGGGCGGGCAGGCACGAAGGIGCCCAGGIICCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.1%; Score 46.8; DB 10; Length: Best Local Similarity 58.7%; Pred. No. 0.0074; Matches 81; Conservative 0; Mismatches 57; Indels
                                        INFORMATION: 8-58-301 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 GAGGCCACCTCTTCCCTG 483
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LOCATION: 659.,2032
NAME/KEY: allele
LOCATION: 4484
                                                                    NAME/KEY: allele
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CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 3099
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                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
OTHEN THORMATION: Incyte ID No. US20020137081A1 300437.18
NAME/KEY: NISURE
LOCATION: 2060
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NAME/KEY: misc_feature
LOCATION: 1076.3075
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
NAME/KEY: exon
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: a, t, c, g, or other US-10-044-090-309
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 8950, Application US/09864761
Sequence 8950, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Fank, David R.
APPLICANT: Banzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 CCAGGTACCGGGGGGGGGGGGAGGCACGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 ACCAGGAGCGAGTTGCACGTGCTCCCTCCCTCCCTCCGCTCAAGGCCAGGAGCTGC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 FGGGACCFGFGFCFGGCAGFGGGAAGGCAGGGGAAGCCFGGTCAGCAGCAGCAGGGFAAAAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 CTGGAGTGCGTGAGAGGGGAAGGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.6; DB 10; Length 599;
Pred. No. 0.0061;
0; Mismatches 115; Indels 0
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.9

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BEATH, SIGNAL = 6.4

US-09-864-761-7244
                                                                         PRIOR APPLICATION NUMBER: PCI/USO1/UG054
PRIOR APPLICATION NUMBER: PCI/USO1/UG065
PRIOR APPLICATION NUMBER: PCI/USO1/UG065
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCI/USO1/UG68
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCI/USO1/UG65
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 7244

LENGTH: 599
                                                      APPLICATION NUMBER: PCT/US01/00664
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Best Local Similarity 49,83
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-09-864-761-8950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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Sequence 7244, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenshenson Warshen G.
APPLICANT: Chen, Wenshen GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 AGGIGGGGCCTCTGCCAGGTACCGGGCGGGCAGGCACGGAGGTGCCCAGGTTCCCGCG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 46.8; DB 10; Length 5566; 58.7%; Pred. No. 0.0076; tive 0; Mismatches 57; Indels 0;
OTHER INFORMATION: 99-13821-332 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: ATTARA

; NAME/KEY: misc_feature

; LOCATION: 10,39,2574,2580,2978,4692,4696,5466

; OTHER INFORMATION: n=a, g, c or t

US-09-416-384A-4
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                                                                                                                                                                                                                                                                                                                             LOCATION: $307.3312
OTHER INFORMATION: potential
NAME/KEY: polyA_signal
LOCATION: 3843.3848
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: potential NAME/KEY: polyA_signal LOCATION: 4524..4529 OTHER INFORMATION: potential NAME/KEY: polyA_signal LOCATION: 5536..5541
                                                                                                                                              LOCATION: 2538...2543
OTHER INFORMATION: potential
NAME/KEY: polyA_signal
LOCATION: 2873...2878
OTHER INFORMATION: potential
NAME/KEY: polyA_signal
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                                                                                  OTHER INFORMATION: potential NAME/KEY: polyA_signal LOCATION: 2538..2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.13
Best Local Similarity 58.77
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: polya_signal LOCATION: 3859..3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-864-761-7244/c
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GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: HUBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aconica X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Barclay, William
APPLICANT: Barclay, William
APPLICANT: Bratt, James
APPLICANT: Rober, Jerry
ITILE OF INVENTION: PUFA POlyketide Synthase Systems and Uses Thereof
FILE REFRENCE: 2997-29
CURRENT APPLICATION NUMBER: US/10/124,800
CURRENT PILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-06-15
PRIOR APLICATION NUMBER: 2001-06-15
PRIOR APLICATION NUMBER: 60/233,269
PRIOR APLICATION DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.9%; Score 45.4; DB 9; Length 3886; Best Local Similarity 63.1%; Pred. No. 0.015; Matches 70; Conservative 0; Mismatches 41; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2518 ACGTGGCAGCGGCGCGCGTCATCGCCGCCACCCTTCTCAGCGGC 2468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 GCCAGGTACCGGGCGGGGCACGCACGGAGGTGCCCAGGTTCCCGCGGAGGC 470
                                                                                              541 GCCGGCAGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23975, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

// LOCATION: (2115)...(2115)

GOTHER INFORMATION: n = a, c, g, or

US-10-124-800-37
                                                                                                                                                                                                                                                                      Sequence 37, Application US/10124800 Publication No. US20020194641A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 3886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Schizochytrium sp
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                                                                                                                                                                                                                                             US-10-124-800-37/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 CTGGAGTGCGTGAGAGAGGGGAAGGGAAGGCCAGAGCAGGAATCAGAGCGAGGCAAA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
CHERR INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 11
US-09-864-761-8950
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                               FILE KEEKENCEA AGONICATOR
CURRENT PERFLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR PILING DATE: 2000-00-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-00-04
PRIOR PILING DATE: 2001-01-30
PRIOR
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ORGANISM: Homo sapiens
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LENGTH: 599
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEALY, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
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             Sequence 22135, Application US/09864761
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ORGANISM: Homo sapiens
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OTHER INFORMATION: MAP TO ACO06757.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4
OTHER INFORMATION: WHIT: M88356.1, EVALUE 1.40e+00
OTHER INFORMATION: EXT_HUMAN HIT: A1016731.1, EVALUE 3.00e-03
US-09-864-761-23975
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         PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-06-30

FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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APPLICANT: HOLD, SHALLON G.
APPLICANT: HEALD, DAVIG R.
TITLE OF INVENTION: HUMAN GENEE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: HUMAN: 1004.05-23
TITLE OF INVENTION: HUMAN: 105-23
CURRENT FILING DATE: 2000-05-26
FRIOR PELLORATION NUMBER: US 60/230, 366
FRIOR PELLORATION NUMBER: PCT/US01/0066
FRIOR PELLORATION NUMBER: PCT/US01/0066
FRIOR APPLICANTON NUMBER: PCT/US01/0066
FRIOR PELLORATION NUMBER: PCT/US01/0066
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                                                 NN: EXPRESED IN BE474, SIGNAL = 47

NN: EXPRESED IN PLACENTA, SIGNAL = 53

NN: EXPRESED IN PHALOO, SIGNAL = 69

NN: EXPRESED IN HBLIO, SIGNAL = 69

NN: EXPRESED IN HBLIA, SIGNAL = 16

NN: EXPRESED IN FETAL LIVER, SIGNAL = 21

NN: EXPRESED IN HELA, SIGNAL = 45

NN: EXPRESED IN HELA, SIGNAL = 45

NN: EXPRESED IN HELA, SIGNAL = 39

NN: EXPRESED IN BRAIN, SIGNAL = 33

NN: EXPRESED IN BRAIN, SIGNAL = 33

NN: EXPRESED IN BOME MARROW, SIGNAL = 21

NN: EXPRESED IN BOME MARROW, SIGNAL = 21

NN: WITHIT: 222828 1, FWALUE 9.000-59

NN: EST_HUMAN HIT: AW409956.1, EVALUE 1.000-58
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                      OTHER INPORMATION: M.
OTHER INPORMATION: E.
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US-09-864-761-2182
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                                                                                                                                             421 CCAGGTACCGGGCGGGCCAGGCACGGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCC 480
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SOFTWARE: Annomax Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 AACGIGGA 202
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US-09-864-761-18923
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LENGTH: 293
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329 ACCAGGAGGAGTIGCACGIGCTCCCTCCCTCCCTCCGCTCAAGGCCAGGAGCIGC 388
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Patent No. US20020081659A1

GENERAL INCRRATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPERENCE: PAIOS

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF ESD ID NOS: 928

SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 52.1%; Pred. No. 0.015;
Matches 98; Conservative 0; Mismatches 90; Indels
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = OTHER INFORMATION: EXPRESSED IN BEALN, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = COTHER INFORMATION: EXPRESSED IN ADUIT LIVER, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2

US-09-864-761-5361
                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 5361
                                                                                             PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
                               APPLICATION NUMBER: PCI/US01/00668
                                                                 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR FILLE AFFERENCE: Aconica-x'-1 of 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-06-36
PRIOR FILLING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2001-01-04
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
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Pred. No. 0.015;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: MAP TO AC009954.1

OTHER INFORMATION: EXPRESSED IN BL474, SIGNAL = 47

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 53

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 69

OTHER INFORMATION: EXPRESSED IN HBLARY, SIGNAL = 27

OTHER INFORMATION: EXPRESSED IN HBLARY, SIGNAL = 16

OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 45

OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 45

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 29

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 29

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 33

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 21

US-09-864-761-2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUNG, SIGNAL = 33
BONE MARROW, SIGNAL = 21
                        PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFFWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 2182
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PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 73.79
Matches 56; Conservative
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US-09-864-761-5361
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Pred. No. 0.07;
0; Mismatches 49; Indels 0;
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT Allen, Keith D.
TITLE OF INVENTION: FRANSCENIC MICE CONTAINING NTTP1
TITLE OF INVENTION: PHOSPHATASE GENE DISRUPTIONS
FILE REFERENCE: R-690
CURRENT APPLICATION NUMBER: US/10/005,858
CURRENT PILLING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/251,802
PRIOR FILLING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3
SCFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2453
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59.5%;
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Best Local Similarity 59.58
Matches 72; Conservative
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                                                                         199 AAGGNGANGGA 209
                                      542 GCGGGCAGGAA 552
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US-10-005-858-1
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APPLICANT: Bayet, John C.
APPLICANT: Bayet, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAI DEPOSITION
FILE REPERBENCE: 16511.066/37-21(10298)C
CURRENT APPLICATION NUMBER: 105/09/960,352
CURRENT FILING DAIE: 2001-09-24
SEQ ID NOS: 15112
SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATION: (51), (100), (106), (118), (121), (193)...(194), (203), (206), LOCATION: (211), (214), (225) OTHER INFORMATION: unsure at all n locations OTHER INFORMATION: clone ID: 64-LIB3057-019-Q1-K1-H8
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49.7%; Pred. No. 0.026;
tive 0; Mismatches 96; Indels 0
                                                                                                                                                                                                                                                                                            Score 43; DB 10; Length 527;
Pred. No. 0.028;
1; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 CTGGAGTGCGTGAGAGGGGAAGGGAGGAAGGCCAGAGCAGGAATCAG 529
                                                                                                                                                                                                                ; LOCATION: (507)
; OTHER INFORMATION: n equals a,t,g, or
US-09-925-297-272
                                                                                                                      OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 14967, Application US/09960352; Patent No. US20020137139A1
; EBERRAL INFORMATION:
; APPLICANT: Warren, Wesley C.
                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature
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56.8%;
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Matches 95; Conservative
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Best Local Similarity 56.89
                                                                             NAME/KEY: misc feature LOCATION: (413)
                                          ORGANISM: Homo sapiens
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US-09-960-352-14967
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                          TYPE: DNA
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        LENGTH:
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Perfect score:

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Scoring table: Sequence:

Database

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM.1840 row: K column: 8
Seq primer: M13RP1 reverse primer (ABI).
B1756040 603030386
B6499418 60246648
B0929418 AGENCOURT
AL053013 Drosophil
AL054280 Drosophil
AL05652 Drosophil
AL05662 Drosophil
AL05662 Drosophil
AL05663 Mrs Albis S9
B1647708 603191859
AA833497 NHTB03a60
                                                                                                     AL237391 ALD34911
BM653599 AGENCOURT
BM810024 AGENCOURT
AL104949 Drosophil
AG060189 Pan trogl
AL2200 HWM02LcD.
AL597104 DKFZp313G
AG06530 Pan trogl
AL65775 Drosophil
AL065775 Drosophil
AL065775 ST637-3-0
AL578905 AL578905
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AL098770 Drosophil
AL572608 AL572608
B1951298 HVSME1002
AG131468 Pan trog1
AL513867 AL513867
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AG043036 Pan trogl
AL301850 Tetradon
AG154064 Pan trogl
AG171092 Pan trogl
BG74244 60263560
BG55144 1025606.x
AL078250 Drosophil
BQ940345 AGENCOURT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhesus monkey.
Macaca mulatta
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 636)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ807824 636 bp mRNA linear EST 3
NISC_kkl0f04.yl NCI_CGAP_Brn72 Macaca mulatta cDNA clone
IMAGE:5331199 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                          CNSOO6N3
AV704516
B189255
AL578905
BQ706827
AG043036
CNSO4PWH
AG171092
BG742444
BG742444
CNSOOROW
BQ940345
                                                                                                                                                      CNSOOKXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca.
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                                                                                                       RESULT 1
BQ807824/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
 BQ807824 NISC_KK10
BQ435307 AGENCOURT
AA904435 OK07911.s
AA889105 am38h04.s
AL708543 DKFZ6666B
BI819086 603033444
                                                               2003, 21:14:32 ; Search time 2221.92 Seconds (without alignments) 4781.561 Willion cell updates/sec
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        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                       16154066 segs, 8097743376 residues
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BQ435307
AA904435
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AL708543
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                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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em_esthu:*
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No. Result

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FEATURES

Query Match

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BASE COUNT ORIGIN

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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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/clone="IMAGE:1507172"
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  Email: cgapbs-r@mail.nih.gov
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AA904435.1 GI:3039558
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Matches 144; Conservative
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ORIGIN
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VERSION
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AUTHORS
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AA904435
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SOURCE
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                                                      /db_xref="taxxon:9544"
/clone="IMAGE:5331199"
/clone="lib="NCI_CGAP_BIN12"
/tissue_type="hypothalamus"
/tab_host="layl00 (phage-resistant)"
/lab_host="layl00 (phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6.ccdb; Site_1:
NotI; Site_2: EcoRy; Cloned unidirecthonally. Primer:
Oligo dT. Average insert size 2.2 kb. Constructed by
Invitrogen. Note: this is a NCI_CGAP Library."
81 a 210 c 190 g 155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ435307 930 bp mRNA linear EST 24-WAY-200
AGENCOURT_7926752 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 930) MIH-MGC http://mgc.noi.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 GGGAGGAAGGCCAGAAGCAGGAATCAGAGCGAGGCAAAGGCGGGCAGGAACTANGAGAATG 563
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    145 GABABARGGACAATAGCCAATGTGTACACTTTTTATAAAAACCACCCTCCAAGGACCAGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                           564 GAAAAACAAACCAATCTCCTGTTGAGCAAAGCCTTCCACAACCACCCCCCCAAAGGACCAGT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTGGCCCTCTCTCCGGTGCCCACAGACATCCACAGGCCCCAAAGAATCAGGGATTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGGTGCCCAGGTTCCCGCGGAGGCCACCTCTTCCCTGGAGTGCGTGAGAGAG-GGGAA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 ACSGCGGGAGGCGGCCGGGAAAAANTCTCGGGGCTGTGGGGGTCNCCCTGGCACCAGC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 ACGGTGGGAGGCGGCCGGGAAAGAGAGTCGCGGGGCTGTGGGGGGTCGCCCTGGCACCAGC
                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                               58.6%; Score 384.4; DB 14; Length 636; ilarity 86.9%; Pred. No. 9.1e-85; Conservative 1; Mismatches 60; Indels 6;
                                         /organism="Macaca mulatta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624 CGGGGTCCCAAGCCCCACCGCGAGACCCCGC 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGGTCCCGAGCCCCATCGAGAGCCGGC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ435307.1 GI:21174383
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Matches 444; Conserv
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RESULT 2 BQ435307

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ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

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EST 09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE.6160773"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab.host="melanotic melanoma"
/lab.host="melanotic melanoma"
/lab.host="melanotic melanoma"
/lab.host="melanotic melanoma"
/lab.host="melanoma"
/lote="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 270)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Bmail: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (infedimage.llnl.gov) for further information.
Insert Length: 437 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 232.

1. .270
Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CLONE Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov. p column: 22

High quality sequence stop: 607.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 AAGGCGGACGTGAAGCATCTACAAAGGAGGAGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AAGGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 TGCACAAGCCAGAGCAATCGAACGGTTCTGAGTCATCTGCCGGAAGCCTTGCCCTCAATC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%; Score 142.8; DB 14; Length 98.6%; Pred. No. 6.1e-25; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 others
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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ok07g11.s1 Soares_NFL_T_GBC_S1 Hc
IMAGE:1507172 3', mRNA sequence.
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Gaps

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boll bp mRNA linear EST 22-MAR-2002 DKF2p686B1453_r1 686 (synchym: hlcc3) Homo sapiens cDNA clone DKF2p686B1453 5', mRNA sequence.
AL708543 GI:19691898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 601)

Wambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.
EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)

Contact: Wambutt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the S' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ): Emails s.wiemann@dKfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKEZP686B1453) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
       726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 61 c 63 g 46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AATCAAGGCGGACGTGAAGCATCTACAAAGGAGAATAGTCAAAGCAGCAGCGGCGGCG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 GTGCCCACAGACATCCACACAG-GCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GTGCCCGCAGACATCCACACAGAGCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATC 123
                                                                                                                                                                                                                                                                                                                 162 CAATGTGTACACTTTTTATAAAAACCACCTCCAAGGACCAGGCACTGGCCCTCTCTCCG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AATCAAGGCGGACGTGAAGCATCTACAAAGGAGGAATAGTCAAAGCAGCGCGGCGG 60
                                                                                                                                                                                                                                                                                                                                                    4 CAATGIGTACACTTTTTATAAAAACCACCTCCAAGGACCAGGCACTGGCCCTCTCTCCG 63
                                                                                                                                                                                                                                                 1; Indels 1;
                                                                                                                                                                           Length 244;
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/db_xref="taxon.9606"
/db_xref="bKF26666B1453"
/clone=lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 16.3%; Score 107; DB 9; I al Similarity 100.0%; Pred. No. 4.4e-16; 107; Conservative 0; Mismatches 0;
                                                                                                                                                                               Score 126.4; DB 9 Pred. No. 6.4e-21;
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                                                                                                                                                                                                                                          0; Mismatches
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/lab_host="DH10B"
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                                                                                                                                                                               19.3%;
98.6%;
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Best Local Similarity 98.65
Matches 138; Conservative
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                                                                         74 a
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                                                                         BASE COUNT
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AL708543
LOCUS
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/note="Organ: pooled; Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Bqual amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the asme 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, CASTON CONTRACTION OF THE PROPERTY OF THE PROPERT
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royally-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 482 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 192.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 GTGCCCACAGACATCCACACAGGCCCCAAAGAATCAGGGATTGCACAAGCCAGAGCAATCG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GIGCCCGCAGACAICCACACACGCCCAAAGAAICAGGGAITGCACAAGCCAGAGCAATCG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.9%; Score 137.4; DB 9; Length 2
Best Local Similarity 99.3%; Pred. No. 1.2e-23;
Matches 138; Conservative 0; Mismatches 1; Indels
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/lab_host="DH10B"
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66 c 74 g 53 t
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/db_xref="taxon:9606"
/clone="IMAGE:1471063"
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SOURCE ORGANISM

KEYWORDS

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 6 BI819086

ACCESSION

VERSION

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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_1 & BCORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 Kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIHMGC Library."
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602546648F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669282 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota, Matazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 896)
                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

1 (bases 1 to 742)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at:
http://image.lnl.gov
Plate: LlaM11502 row: 1 column: 22
High quality sequence stop: 742.
1. 742.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
CNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammallan Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 76.4; DB 13; Length 742; 98.7%; Pred. No. 1.7e-08; ative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_114"
/lab_host="DH10B"
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Context: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 98.77
Matches 77; Conservative
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BG499418
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pCMV-SPORT6; Site.1: NotI: Site.2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27;
nale lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (BCoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this a NHH_MGC Library."
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                                                                                                                           707 bp mRNA linear EST 04-OCT-2001 603033444F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5174458 5', BI819086
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: ILAMI1434 row: h column: 11
High quality sequence stop: 697.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHH-MCC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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61 CGGCGGCGGCAGCAGCAGCAGCAGGAGGTGGGGGCCTCTGCCAG 107
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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B1756040
B1756040.1 GI:15747618
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/clone_lib="RPCI-98"
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Drosophila melanogaster
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( passas 1 to 925)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC); Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aarron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPOI-98 and was constructed by partial Ecogal cibrary is named RPOI-98 and was constructed by partial Ecogal strain y2; on bw sp. the same strain used for the BDGP's land by the BDGP from the BDGP is a name of the library by and BSC library and the BDGP is a part of the BDGP is a part of the BDGP is a part of the BDGP is a more detailed description of the library and the BDGP is a part of the BDGP is a part of the BDGP is a more detailed description of the library and the BDGP is a part of the B
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally. Primer: Oligo dT.
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Ephydroidea; Drosophilidae; Drosophila.

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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29L07 of RPCI-98 library from Drosophila melanogaster (fruit
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                      |::::: :: |: : : : : : |:| |:| |:| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
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                                                                                                          461 CCGCGGAGGCCACCTCTTCCCTGGAGTGCGTGAGAGGGGAAGGGAAGGCCAGAGC 520
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   463 TASMSSSSACSASASSGCSASSCVAACSSACAGSGASAGSSSSASGSCGAGSSSSAGGS 522
                                                                     401 GCAGGAGGIGGGGCCTCTGCCAGGTACCGGGCGGGGCAGGCACGCAGGTGCCCAGGTTC 460
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Nr. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence TET3 end of BAC # BACRLÖE16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRX cedex - FRANCE (F-mail : seqref@genoscope.cns.fr
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Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Citona intestinalis
library from which the clone was isolated may be contaminated with
cobnas from bacteria or other Eukeryra.
Directional larval conta library originate from Dr. W. Branno,
Stazione A. Dohrn, Naples, Italy, and was prepared in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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                                                                                                                                                                                                                                 447 CCSGGMSASSSSSSGGVSSVSGGRAVGRGRCMCCSMVCCCMCSSMCCSMCCSVSSVCAVC 506
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                                                                                                    Length 844;
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309 c 21 g 12 t 6 others
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                                                                                    Score 56.2; DB 17;
Pred. No. 0.0017;
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                                                                                                                        1 Similarity 18.4%; Pred. No. 0.00741; Conservative 110; Mismatches
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                                                                          346
                                                                                                                                                                                                                                                                        407 GCTGGGGGCCTCTGCCAGGTACCGGGGGGGCAGGCACGGAGGTGCCCAGGTTCCCGCGG 466
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                       287 ITCTGAGTCATCTGCCGGAAGCCTTGCCCTCAATCAAGGCGGACGTGAAGCCATCTACAAA
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                                                                                                                                                                 BIS47708 691 bp mRNA linear EST 05-SEP-2001 603191859F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5263095 5',
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                                                           548 AGGAACTANGAGAATGACSGCGGGAGGCGGCCGGGAAAGAAANTCTCGGGGCTGTGGGGG 607
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1 atcgaacggttctgagtcatct 22
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Submarted (01-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

S. (bases 1 to 19135)

Birren B. Linton L. Wusbaum.C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, M., Beda, F., Boguslavkiy, L., Bowkhalter, B., Brown, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhdy, M., Fortset, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karsta, M., Klein, J., Landroque, K., Lehoczky, J., Levine, R., Klein, J., Landroque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGarth, A., McCarnan, R., Wobheters, R., Maddrin, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J., Riley, R., Rogov, P., Rolman, D., Roy, A., Santos, R., Schauer, S., Stencer, B., Stange-Thomann, N., Stolanovic, N., Tiraver, R., Travers, M., Tisgillo, J., Tasker, R., Vola, Milson, B., W.X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
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Submitted (17-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, 05A
On Jan 16, 2000 this sequence version replaced gi:6514043.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
   Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Liboczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McFann, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramainn, A., Testaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wulk, N., Wann, D., Ye, W.J. and Zody, M., Wagner, A., Macheller, J., Wagner, A., Macheller, J., Wagner, A., Macheller, J., Wagner, A., Wag
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project information
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/clone_lib="RPC1-11 Human Male BAC"
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complement(1673. .1726)
/note="Single-stranded coverage."
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complement(1724. .1770)
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Center clone name: 793_J_2
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1632. .1687
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/rpt_family="L1"
708. .1353
/rpt_family="L1"
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1 (bases 1 to 656)

Del-Pavero,J., Raeymaekers,P. and Van Broeckhoven,C.
Mood disorder gene
Patent: MO 9932643-A 12 01-JUL-1999;
BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS PETER (BE); VLAMS INTERNIVI INST BIOTECH (BE)

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Homo sapiens chromosome 18, clone RP11-793J2, complete sequence.
ACO09802
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dakrellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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9216. .9496

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9961. .1026

9961. .1026

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/rpt_family="THEIC".1155)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases I to 1917)

Rattori, M., Ishi, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakai, Y. Homo. Saplena 191793 genomic DNA of 18q22

Lubushished Only in Database (2000)

2 (bases I to 191793)

Rattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

AL Matana, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

AL Matanabe, H. and Sakaki, Y. Direct Submission

AL Submitted (24 APR-200) Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato, Sagamihara, Kanagawa 228-855, Japan (E-mali:hattori@gsc.riken.go.jp,

WRL:http://hpp.gsc.riken.go.jp/, Tel:81-42-778-9923,

On May 30, 2000 this sequence version replaced gi:7649784.
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Homo sapiens DNA, clone:RP11-693A18.
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185299 186320 contig of 1022 bp in length
186421 187601 contig of 1181 bp in length
187702 189099 contig of 1398 bp in length
189200 190576 contig of 1377 bp in length
189207 191793 contig of 1377 bp in length
Sequence updated (26-May-2000).
* NOTE: This is a "working draft' sequence. It currently
* consists of 54 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* trus of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                    100 bp

37797 37896: contig of 8857 bp in length

45644 45743: contig of 7747 bp in length

4574 45743: qap of

4574 53200: contig of 7747 bp in length

4574 53200: contig of 7457 bp in length

53201 53301 qap of

53467 59566: contig of face
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146412 148694: contig of 2283 bp in length
146895 148794: gap of 100 bp
148795 151551: contig of 2757 bp in length
151552 151651: gap of 100 bp
151652 153471: contig of 1820 bp in length
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19551 28739; contig of 9189 bp in length
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95358 99276; contig of 3919 bp in length
99277 98376; gap of 100 bp
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132976 136718; contig of
136719 136818; gap of
136819 140204; contig of
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140205 140304: gap of
140305 143312: conti
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                                                                                                                                           Insert size: 186493; sum-of-contigs
Quality coverage: 4.60x in Q20 bases; sum-of-contigs
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Birren,B., Linton,L., Nusbaum,C., Lander,B., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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HOMO Sapiens chromosome 18 clone RP11-693A18 map 18, WORKING DRAFT
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
                                                                                     Genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                          Submitted (27.APR-2000) Whitehead Institute/MIT center for Research, 320 Charles Street, Cambridge, MA 02141, USA On May 24, 2001 this sequence version replaced gi:13560423. Smit. A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-693A18
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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/organism="Homo sapiens"
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Table Onpublished

Table Onpublished

Sharen, Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Andersen, S., Baldwin, J., Barna, N., Bastien, Y., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, Y., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahan, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lilev, T., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lander, E., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPherers, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, T., O'Connor, T., O'Nonnor, T., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Stantos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
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157931 160335: contig of 23
160336 160435: gap of 15
160436 161957: contig of 15
161958 162057: gap of 15
161958 164115: contig of 20
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66475 168634: contig of
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AP001503
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                         Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagfos, B., Haeford, A., Horton, L., Hulme, W., Liley, I., Johnson, R., Jones, C., Karatas, A., Laxocque, K., Lamazres, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matherin, P., MacCarthy, M., McEwan, P., McKernan, K., Morphy, T., Maylor, J., Meneus, L., Minova, P., Minova, T., Minova, T., Wlender, R., Maylor, J., Maylor, J., Morphy, T., Naylor, J., Moupe, C., Norbu, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Pierre, N., Pollara, V., Raymond, C., Retta, R., K., Schauer, S., Schupe, S., Schupe, S., Schupe, C., Spencer, B., Stange-Thomann, N., Stalay, R., Stange-Thomann, N., Stalay, R., Takamas, J., Tesfaye, S., Theodore, J., Firavers, M., Traylifo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M.J., Young, G., Zainoun, J., Zembes, L., Zimmer, A. and and Zoy, M., Young, G., Zainoun, J., Lender, M., Takan, A., Takamas, J., Tesfaye, Zainoun, J., Lender, A., Takan, A., Ye, M.J., Young, G., Zainoun, J., Lender, M., Takan, A., Takamas, J., Tesfaye, Zainoun, J., Lender, M., Takan, A., Takamas, J., Ye, M.J., Young, G., Zainoun, J., Lender, M., Takan, A., Takan, A., Ye, M.J., Young, G., Zainoun, J., Lender, M., Takan, A., Tak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON May 23, 2001 this sequence version replaced gi:13621272. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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Insert size: 201034; sum-of-contigs
Quality coverage: 11.3 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45184 45283; gap of 45184 45283; gap of 45184 45283; gap of 45185 bp in length 46769 46868; gap of 100 bp 46869 47961; contig of 109 bp in length 47962 48061; gap of 100 bp 47962 49643; contig of 1582 bp in length 4964 49743; gap of 100 bp 4974 51393; contig of 1560 bp in length 51394 51493; gap of 100 bp 51394 51493; gap of 5100 bp 51394 51493; gap of 512038 bp in length 51394 51493; gap of 512038 bp in length 51394 51493; gap of 512038 bp in length
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74532 127710: contig of 53079 bp in length
127711 127810: gap of 100 bp
127811 201734: contig of 73924 bp in length.
Location/Qualifiers
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Web site: http://www-seq.wi.mit.edu
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/organism="Homo sapiens"
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COMMENT

/db_xref="taxon:9606" /chromosome="18"

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momo supperso; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 186351)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Published Only in DataBase (2000)

2 (bases 1 to 186351)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
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APO01503
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Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://App.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
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------- Summary Statistics
Sequencing vector: PCR products; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708 others
                                                   /clone_lib="RPCI-11 Human Male BAC"
1. .45183
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Contact: hattori@gsc.riken.go.jp
------ Project Information
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61611 a 39444 c 39572 g 60399 t
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48062. 49643.
Anotes" assembly_fragment"
4974. 51393
Anotes" assembly_fragment"
51494. 74531
Anotes" assembly_fragment"
74632. 127710
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46869. .47961
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                            /clone="RP11-693A18"
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vector_side:left"
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183745 184761: contig of 1017 bp in length
184762 184861: gap of 100 bp
184862 186351: contig of 1490 bp in length.
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56377 a 36459 c 35952 g 55363 t
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183745 184761
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                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
               Assembly program: Phrap; version 0.990329
Consensus quality: 162162 bases at least Q40
Consensus quality: 175389 bases at least Q30
Consensus quality: 181326 bases at least Q20
Insert size: 184151; sum-of-contigs
Quality coverage: 4.54x in Q20 bases; sum-of-contigs
Chemistry: Dye-terminator ET-amersham; 100% of reads
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135845 145972: contig of 10128 bp in length
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1270: gap of 100 bp
156398: contig of 3128 bp in length
1698: gap of 100 bp
161724: contig of 5226 bp in length
1824: gap of 100 bp
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/note="GPAIL 2 excellent exon, frame 1"
41668. 41709
/note="(GT)21"
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/rpt_family="Alu"
41063. .41227
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                                        complement(9224. .9512)
/rpt_family="Alu"
9547. .9770
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.xpt_family="Alu"

28720. .29000

/rpt_family="Alu"

28983. .29004

/note="(A)22"
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/rpt_family="Alu"
complement(23851.
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family-"Alu"
8. .18524
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/rpt_family="MIR"
complement(19388.
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10027. .10567
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/rpt_unit=A
29085. .29200
/rpt_family="L1"
30322. .30591
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30589. .30644
/note="(AAAT)14"
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33057. .23365
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family="L1"
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/note="(T)21"
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Homo sapiens chromosome 5, PAC clone 248b21 (LBNL H141), complete
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1 (bases 1 to 95448)
1 (bases 1 to 95448)
1 (bases 2 to 95448)
1 (bases 2 to 95448)
1 (bases 3 to 9574; Secian, M., Shiang, R. and Wasmuth, J.J.
2 high-resolution physical and transcript map of the Cri du chat region of human chromosome 5p
6 Genome Res. 7 (8), 787-801 (1997)
9267803
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Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radmer,K., Miguel,T., Willer,C., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.
Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System Unpublished
                                                                                        Gaps
                                        Score 20.4; DB 2; Length 186351;
Pred. No. 3.2;
0; Mismatches 1; Indels 0;
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complement(7124. .7257)
/note="GRAIL 2 excellent exon, frame l"
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/note="GRAIL 2 excellent exon, frame
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/rpt_family="MER7"
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/rpt_family="L1"
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/clone="248b21"
                                                                                                                                   1 ATCGAACGGTTCTGAGTCATCT 22
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AC005572.1 GI:3510228
                                        ch 92.7%;
11 Similarity 95.5%;
21; Conservative (
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Ricke, D.O.
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                                          Query Match
Best Local Similarity
Matches 21; Conserv
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ORIGIN
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Submitted (03-JUN-2002) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr wav.genoscope.cns.fr)

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence.

Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
                                                                                                                                         CNSO8C9K
ONYZA SATIVA Chromosome 12 clone OSJNBb0090H23, *** SEQUENCING IN PROGRESS ***, 11 ordered pieces.
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzaa.

1 (Dases 1 to 12409); Cattolico, L.; Demange, N.; Wincker, P.; Segurens, B.; Pelletier, B.; Scarpelli, C.; Salanoubat, M.; Oryza sativa chromosome 12 sequencing Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contigs composition:
1707 bp contig from 1 to 1707
13399 bp contig from 12017 to 21574
22666 bp contig from 12017 to 21574
22666 bp contig from 22675 to 44280
9040 bp contig from 23675 to 44280
9040 bp contig from 23675 to 10251
20348 bp contig from 23651 to 73868
9188 bp contig from 23551 to 10351
6512 bp contig from 102518 to 109129
8922 bp contig from 102518 to 109129
8922 bp contig from 10352 to 104092.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 11 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
** 1708 1807: gap of 100 bp
** 15217 15216: gap of 100 bp
** 15217 22157: contig of 6358 bp in length
** 21575 44281 app of 100 bp
** 44281 44380: contig of 22606 bp in length
** 44281 44380: contig of 22606 bp in length
** 44381 44380: contig of 22606 bp in length
** 5420: contig gap of 100 bp
** 44381 53420: contig of 05040 bp in length
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                                                                                                                                                                                                                         AL732645.
AL732645.1 GI:21326737
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
44786 TCTAAGGGTTCTGAGTCATCT 44766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 124092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                    Oryza sativa.
                                                                                               RESULT 9
CNSO8C9K
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
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AUTHORS
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'note="99% identity B07638 (exon trapped product)"
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                                                                                                                    /note="GRAIL 2 excellent exon, frame 0"
complement(49858..50004)
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complement(50482..50554)
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/rpt_family="L1"
/rpt_family="L1"
complement(51301..51570)
/rpt_family="L1"
53075..53337
                                                                                                                                                                                                                                                                                                                                                                  rpt_family="Mirla"
complement(59112. .59259)
note="GRALL 2 excellent exon, frame 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_type=tandem
/rpt_unit=AATA
66046. .66147
/note="GRAIL 2 excellent exon, frame 0"
68813. .68852
/note="(ATCT)10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(73385. .73695)
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complement(73801. .73925)
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/db xref="dbEST:AA862321"
/3944. .94270
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/5779. .77132
/rpt_family="THE1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(82147. .82531)
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complement(82908. .83342)
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83752. .84040
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/rpt_family="Alu"
81076. .81185
/note="RRAIL 2 excellent ex
complement(81404. .81485)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_unit=Arcr
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72177. .72322
                                                                        /rpt_family="Alu"
complement(48265. .48384)
                       /db_xref="dbSTS:G31407"
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61998. .62033
/note="(AATA)9"
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84023. .84044
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/note="(AC)18"
/rpt_type=tandem
/rpt_unit=AC
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/rpt_unit=A
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Valence Submission (24-NOV-2000) Genome Sequencing Center, Washington Submitted (24-NOV-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, On Nov 30, 2000 this sequence version replaced gi:11323446.
                                                                                                                                                                                                                                                                                                                                                                                                        ACO84869 176641 bp DNA linear HTG 11-MAR-2001
Homo sapiens chromosome RPCI-11 clone RP11-508E4, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176641)
                                                                                                                                                                  Gaps
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                                                                                                            Score 17.8; DB 10; Length 175238;
Pred. No. 1.1e+02;
0; Mismatches 2; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Mi3; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142830 bases at least Q40
Consensus quality: 154079 bases at least Q30
Consensus quality: 156059 bases at least Q30
Insert size: 183000; agarose-fp
Insert size: 172341; sum-of-contigs
Quality coverage: 2.73 in Q20 bases; sum-of-contigs
Quality coverage: 3.02 in Q20 bases; sum-of-contigs
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contig of 1270 bp in length
contig of 1233 bp in length
contig of 1233 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
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Web site:http://genome.wustl.edu/gsc/index.shtml
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     /clone_lib="RPCI-23"
45250 a 39075 c 40628 g 50285 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, 44 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                 DD 11296 TCGATCGGTTCTGAGCCATCT 11316
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AC084869.2 GI:11465172
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                                                                                                         Match 80.9%;
Local Similarity 90.5%;
Les 19; Conservative C
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3037:
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Submitted (20-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Direct Submission

Submitted (20-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

hunquery(sanger.ac.uk Clone requests: clonerequest(sanger.ac.uk On Feb 22, 2002 this sequence version replaced q1:17381401.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations. Where differences are found these are annotated as variations. The sequence with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPRON; PIL:, TREMEL, Wenner and WORMPEP information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL606903 175238 bp DNA linear ROD 20-FEB-2002 Mouse DNA sequence from clone RP23-27813 on chromosome 4, complete
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 175238)
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from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               80.9%; Score 17.8; DB 2; Length 124092; 90.5%; Pred, No. 1e+02; ive 0; Mismatches 2; Indels 0;
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This sequence is the entire insert of clone RP23-278I3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         /clone_lib="OSJNBb"
27560 c 27075 g 34750 t 1000 others
/organism="Mus musculus"
                                                                                                                                                                                /cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
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/chromosome="4"
/clone="RP23-27813"
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                                                                                                                                                                                                                                                                           /chromosome="12"
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Matches 19; Conservative
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Query Match 80.9%; Score 17.8; DB 2; Length 176641; Best Local Similarity 90.5%; Pred. No. 1.1e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0; 1518 150517: gap of unknown length
1518 158426: contig of 7909 bp in length
1427 158526: gap of unknown length
1557 167566: contig of 9040 bp in length
1557 167566: gap of unknown length
1567 17661: contig of 8975 bp in length
1667 176641: contig of 8975 bp in length.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as runs of M, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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1112: gap of unknown length
2405: contig of 1293 bp in length
2505: gap of unknown length
3686: contig of 1181 bp in length
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5018: contig of 1059 bp in length
5118: gap of unknown length
6177: contig of 1059 bp in length
6277: gap of unknown length
7622: contig of 1059 bp in length
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11066: contig of 1826 bp in length
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Consensus quality: 137677 bases at least Q40
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Contact: hgsc-help@bcm.tmc.edu
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Buray, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alstray, D. M., Adams, C., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barabaria, J., Benden, J., Burad, R., Barak, M., Barak, D., Barabaria, J., Benden, J., Burad, M., Eryant, N.P., Bulay, C., Burch, D., Bulay, C., Burch, D., Bulay, C., Burch, D., Carter, M., Cavazos, S.R., Chacko, J., Charez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Davis, C., Dany, A.L., Dady, T., Dink, T., Dink, J., Davila, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dedarich, D.A., Deland, C.D., Cox.C., Coyle, M.D., Dath, R.J., Duthin, K.J., Douthwaite, K.J., Drager, H., Dangan-Rocha, S., Durbin, K.J., Barlis, T., Ferraguto, D., Edwards, C., Eschis, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Edwards, M., Garner, T., Gazza, M., Gill, R., Gobisi, A., Gao, J., Garner, H., Havlak, P., Hawes, A., Hennadez, C., Harris, K., Harris, M., Hollyk, S., Hume, J., Hollins, S., Hume, J., Jai, Y., Johnson, R., Jollivet, S., Joudah, S., Kallson, E., Howard, S., Huber, J., Hullyk, S., Hume, J., Jai, Y., Johnson, R., Jollivet, S., Joudah, S., Karlson, E., Kallson, E., Kallson, E., Kallson, E., Kallson, E., Kallson, E., Kallson, E., Martinez, E., Savery, G., Oragunye, N., Oriedo, M., Payton, B., Peerz, J., Raves, A., Ravison, E., Savery, G., Scher, S., Sonaike, T., Sparsk, A., Tamerisa, A., Tamerisa, A., Tangy, H., Suther, S., Sonaike, T., Sparsk, A., Tanerisa, A., Tangy, H., Suther, S., Wolmen, S., Warten, A., Wallen, S., Walliamson, M., Willes, M., Walle, S., Marren, R., Walliamson, S., Walliamson, M., Walles, M., Walles, M., Walles, M., Walles, M., Walles, M., Walles, M., Walles
                                                                                                                                                                                                                ACLIBES 178103 bp DNA linear HTG 18-JUL-2002 Rattus norvegicus clone CH230-246K21, *** SEQUENCING IN PROGRESS ***, 47 unordered pieces.
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Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                       Db 76238 TCTAAGGGTTCTGAGTCATCT 76218
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Homo sapiens chromosome 5 clone CTD-2202L20, complete sequence.
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Insert size: 203349; 5.9% error; agarose-fp
Quality coverage: 11.87x in Q20 bases; sum-of-contigs Quality
coverage: 13.78x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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Pred. No. 1.1e+02;
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56012 c 56424 g 59522 t
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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
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1. .138728
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Matches 19; Conserv
   house mouse.
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HTG; HTGS_PHASEL; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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/db_xref="taxon:10116"
/clone="CH230-246K21"
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Matches 19; Conservative
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 192082)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 258929)
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DOB Joint Genome Institute and Stanford Human Genome Center.
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.6.
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90.5%; Pred. No. 1.1e+02;
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/db_xref="taxon:9606"
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Gaps

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Indels

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cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Mar 21, 2002 this sequence version replaced gi:1753431.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plaamid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
SWISSPROT; TE:, TREMBL; WHORMERP; Information on the WORMERP
database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-144020 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the entire insert of clone RP23-144020 The true right end of clone RP23-36P22 is at 1079 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Single clone region. Assembly confirmed by restriction digest data." 45197 c 45566 g 51180 t
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/db_xref="taxon:10090"
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Arabidopsis thalia
Arabidopsis thalia
Human immunophilin
Partial sequence o
Human kappa opioid
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Eucalyptus grandis
Eucalyptus grandis
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Human Oestrogen re
Haemophilus influe
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Synthetic Hydroxym
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Bacillus lichenifo
Arabidopsis thalia
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AAK52200
AAC59479
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AAC39132
AAT18796
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AAD11038
ABL28558
AAC78150
AAS23393
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AAC35713
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AAN82030
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AAA79313
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AAS43104
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ABL07834
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AAC43261
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ABL71087
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AAX88557 standard; DNA; 22
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                          Synthetic
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EST clone BV27.
Arabidopsis thalia
Human ORFX ORF2808
Helminth aminopept
Helminth aminopept
Helminth aminopept
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                                                                                                       (without alignments)
4746.432 Million cell updates/sec
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/SIDS2/gcgdata/geneseqr/geneseqn_emb1/RM1990.DAT:*
/SIDS2/gcgdata/geneseqr/geneseqn_emb1/RM1991.DAT:*
/SIDS2/gcgdata/geneseqr/geneseqn_emb1/RM1992.DAT:*
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/SIDS2/gcgdata/geneseqr/geneseqn_emb1/RM1995.DAT:*
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                                                                                         January 9, 2003, 19:55:35; Search time 10.4381 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSZ/gcgdata/geneseg/genesegn-embl/NA1980.DAT:*/SIDSZ/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*/SIDSZ/gcgdata/geneseg/genesegn-embl/NA1982.DAT:*/SIDSZ/gcgdata/geneseg/genesegn-embl/NA1982.DAT:*/SIDSZ/gcgdata/geneseg/genesegn-embl/NA1983.DAT:*/SIDSZ/gcgdata/geneseg/genesegn-embl/NA1984.DAT:*/SIDSZ/gcgdata/geneseg/genesegn-embl/NA1984.DAT:*
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                        2185239 seqs, 1125999159 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

N_Geneseq_101002:*

Database

1 atcgaacggttctgagtcatct 22

US-09-581-500B-13

Title: Perfect score:

Sequence:

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The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers blass8 and b185979 to identify a human gene associated with a mood disorder or related disorder. Axx88542 to Axx88705 represents human chromosome 18q XaC clones and primers corresponding to them, used in the exemplification of the present invention. YaC clones comprising a portion of the region of human chromosome 18q between markers D18589 and closed to identify at least one human gene associated with a mood disorder or related disorder. The mood disorder or related disorder. The mood disorder or related closen from the Diagnostic and Statistical Manual of Mental closeders, is chosen from the Diagnostic and Statistical Manual of Mental closeders, version 4 (DSM-IV) taxonomy. This includes mood disorders (296.Xx, 300.44, 311, 301, 13, 297.3), 298.9), anxiety disorders (300.Xx, 309.81, 308.3), adjustment disorders (309.Xx) and personality disorders (codes 301.XX). Probes derived from genes associated with the mood clisorder or related disorder can be used to detect pathological mutations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual come mood disorder or related disorder. The nucleic acids and proteins of the human gene can be used to treat mood disorders and related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 22; DB 20; Length 656; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
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Treacy M;
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Best Local Similarity 100.
Matches 22; Conservative
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Racie LA, Spaulding V,
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                                                                                                           The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers bl8568 and D185979 to identify a human gene associated with a mood disorder or related disorder. AAX88542 to AAX88705 represents human chromosome 18q TAC clones and primers corresponding to them, used in the exemplification of the present invention. TAC clones comprising a mod disorder or related disorder. The mood disorder or related disorder. The mood disorder or related disorder. The mood disorder or related conson from the Diagnostic and Statistical Manual of Mental Colorates, version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4, 311, 301, 13, 295.70), Schizophrenia and related clisorders (296.XX, 300.4, 311, 308.3), adjustment disorders (309.XX) and personality disorders (codes 301.XX). Probes derived from quenes associated with the mood clisorder or related disorder can be used to detect pathological antibodies can be used to determine the susceptibility of an individual content of the human gene can be used to treat mood disorders and related disorder. The mood disorders and related disorder. The mood disorders and related disorder. The nooled content or related disorder. The nooled content or related disorder. The nucleic acids and proteins and related disorder or related misorder. The nucleic acids and proteins
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           Detecting nucleotide triplet repeats in human chromosome 18q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 5 A; 5 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Fig 15a; 87pp; English
                                                                  Claim 29; Fig 15b; 87pp; English.
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es 22; Conserv
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AAX88553;

RESULT 2 AAX88553

Query Match Best Loca Matches

õ g McCoy JM, Merberg D;

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990S-0140823.
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990S-0141287.
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9903-0144086.
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9903-0144333.
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99US-0144335.
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99US-0144632.
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99US-0139899.
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990S-0143542.
990S-0143624.
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99US-0145918
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19-JUL-1999;
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27-JUL-1999;
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01-JUL-1999;
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                                                          25-MAY-1999;
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6-JUN-1999
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15-JUL-1
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29-JUN-1
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   all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
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                                                                                                                                                                         Score 17.2; DB 20; Length 486; Pred. No. 35;
                                                                                                                                                                                               Indels
                                                                                                                                                  Sequence 486 BP; 145 A; 114 C; 110 G; 116 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 33540.
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                   AAC41897 standard; DNA; 1164 BP
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990S-0130510.
990S-0130891.
990S-0131449.
990S-0132048.
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99US-0132486.
99US-0132487.
99US-0132863.
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990S-0134218.
990S-0134219.
990S-0134221.
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126785.
99US-0127462.
99US-0128714.
                                                                                                                                                                       78.2%;
Local Similarity 86.4%;
nes 19; Conservative
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                                                                                                                                                                                                                      1 ATCGAACGGTTCTGAGTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                17-0CT-2000
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Matches
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990x-0145919. 990x-014598. 990x-0146386. 990x-0146388. 990x-0147302. 990x-0147302. 990x-0147302. 990x-0147302. 990x-0147416. 990x-0147416. 990x-0147416. 990x-01474173. 990x-01474173. 990x-014864. 990x-014864. 990x-014864. 990x-0148902. 990x-0149902. 990x-0149902. 990x-0149902. 990x-0149902. 990x-0151066. 990x-0151066. 990x-0151066. 990x-0151066. 990x-0151066. 990x-0151066. 990x-0151080.	905 - 0159331 907 - 0159331 908 - 0159583 908 - 016076 908 - 016076 908 - 016076 907 - 016081 907 - 016081 907 - 016081 907 - 0160981 907 - 0160981 907 - 0160981 907 - 0160981 908 - 0161406
27 - JUL - 1999; 28 - JUL - 1999; 02 - AuG - 1999; 03 - AuG - 1999; 04 - AuG - 1999; 04 - AuG - 1999; 04 - AuG - 1999; 06 - AuG - 1999; 06 - AuG - 1999; 06 - AuG - 1999; 10 - AuG - 1999; 11 - AuG - 1999; 12 - AuG - 1999; 13 - AuG - 1999; 14 - AuG - 1999; 15 - AuG - 1999; 16 - AuG - 1999; 17 - AuG - 1999; 18 - AuG - 1999; 19 - AuG - 1999; 19 - AuG - 1999; 10 - AuG - 1999; 11 - AuG - 1999; 12 - AuG - 1999; 13 - AuG - 1999; 14 - AuG - 1999; 15 - SEP - 1999; 16 - SEP - 1999; 17 - AuG - 1999; 18 - SEP - 1999; 19 - SEP - 1999; 11 - SEP - 1999; 11 - SEP - 1999; 11 - SEP - 1999; 12 - SEP - 1999; 13 - SEP - 1999; 14 - SEP - 1999; 14 - SEP - 1999; 15 - SEP - 1999; 16 - SEP - 1999; 17 - SEP - 1999; 18 - SEP - 1999; 18 - SEP - 1999; 19 - SEP - 1999; 10 - SEP - 1999; 11 - SEP - 1999; 11 - SEP - 1999; 12 - SEP - 1999; 13 - SEP - 1999; 14 - SEP - 1999; 14 - SEP - 1999; 16 - SEP - 1999; 17 - SEP - 1999; 18 - SEP - 1999; 18 - SEP - 1999; 19 - SEP - 1999; 19 - SEP - 1999; 19 - SEP - 1999; 10 - S	#-001-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999 #-007-1999
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                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                   ó;
                                                                                                                                                                                                                                                             Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORFX ORF2808 polynucleotide sequence SEQ ID NO:5615.
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                          DB 21;
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                                                                                                                                                                                                                                                   Score 17.2; DE
Pred. No. 39;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          1 ATCGAACGGTTCTGAGTCATCT 22
| |||| ||||||||||||
201 ACCGAATCGTTCTGAGTCATCT 222
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                                                                                                                                                                                                                                                   78.2%;
nilarity 86.4%;
Conservative 0
                                                                                                                             99US-0161992.
99US-0161993.
99US-0162142.
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                   99US-0161360.
99US-0161361.
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Best Local Similarity
'-has 19; Conserve
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26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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RAC77253
ID AAC77253

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geographical origin. Antigenic fragments of the aminopeptidases encoded by these sequences may be used in vaccines to stimulate immune response against helminth parasites in humans or other animals. These DNA sequences may be incorporated into a virus or microbe and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beptidase genes Hil-3, -2 and -1 respectively. These sequences encode Hillowhich is a protein doublet which shows homolgy to a family of integral membrane aminopeptidases. The differences between these coding sequences can be attributed to different mRNAs of the multigene family, and also to different variants of the Hillonencoding sequence being present at different stages of the life cycle, or in strains differing in geographical origin. Antigenic fragments of the aminopeptidases encoded by these sequences may be used in vaccines to stimulate immune response against helminth parasites in humans or other animals. These DNA sequences may be incorporated into a virus or microbe and used in a similar manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helminth; aminopeptidase; Hl1-3; Hl1-2; Hl1-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAQ52489-91 represent the helminth amino-
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                                                                                                                                                                                      Score 17.2; DB 14; Length 1689; Pred. No. 41;
                                                                                                                                                                                                                                            3; Indels
                                                                                                                                           Sequence 1689 BP; 515 A; 330 C; 419 G; 425 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oliver JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= Aminopeptidase H11-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knox DP, Munn EA, Newton SE,
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
33..3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helminth aminopeptidase H11-1 gene.
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                                                                                                                                                                                                                                            ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ52491 standard; DNA; 3006 BP.
                                                                                                                                                                                                                                                                                                                                         505 ATCGAACGCTTCTGATACATCT 484
                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-GB00943.
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                                                                                                                                                                                             78.2%;
86.4%;
                                                                                                                                                                                                                                                                                            1 ATCGAACGGTTCTGAGTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                   used in a similar manner.
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-386574/48.
P-PSDB; AAR51282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vectors, transformed
in virus or microbe
                                                                                                                                                                                                                 Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9323542-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Graham M,
Smith TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ52491;
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
AAQ52491/c
ID AAQ5249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
    88888
                                                                                                                                                                                                                                                                                              δŏ
                      antidiabetic; hypotensive; dermatological; immunosuppressive; antinhammatory; antibacterial; antiviral; antinhammatic; antithermatory; antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, profit short disease, cardiovascular disease, diabetes mellitus. Appertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, acterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to enhance coagulation, to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAG52498-99 represent cDNA clones of the helminth aminopeptidase gene H11-1. H11-1 encodes H110D which is a protein doublet which shows homolgy to a family of integral membrane aminopeptidases. The differences between these coding sequences can be attributed to different mRNAs of the multigene family, and also to different variants of the H110D-encoding sequence being present at different stages of the life cycle, or in strains differing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helminth; aminopeptidase; Hll-3; Hll-2; Hll-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe; HllOD; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation
    immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.2; DB 21; Length 1522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1522 BP; 537 A; 352 C; 324 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Graham M, Knox DP, Munn EA, Newton SE, Oliver JJ;
Smith TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helminth aminopeptidase H11-1 clone AustB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AGRI-) AGRIC & FOOD RES COUNCIL.
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ID AAQ52498 standard; CDNA; 1689 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 5; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 ACCGAACAGTICIGAGTCATTI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.2%;
86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 86.4 ses 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-386574/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in virus or microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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us-09-581-500b-13.rng

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AAQ52500;

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Gaps

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Indels

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The present invention provides the protein and coding sequences of the human 07G627 oncogene. This gene is found at the HPC1 region of circonosome 1. The sequences can be used in the diagnosis and identification of treatments for prostate cancer. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human prostate cancer marker gene termed as 0.7{\rm CG}2.7~{\rm gene}, useful for screening mutations in the gene in diagnosis of a predisposition to
                                                                                                                                                                                                                                                                                                           Human; 07CG27 gene; chromosome 1; HPC1 region; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10347 BP; 3325 A; 2451 C; 2229 G; 2342 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rommens JM;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.2; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product "07CG27 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tavtigian SV, Swedlund B, Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
225..8684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 79-91; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                BP.
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                                                                      1429 ATCGAACGCTTCTGATACATCT 1408
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                                                                                                                                                                AAF28060 standard; cDNA; 10347
                                  22
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86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCGAACGGTTCTGAGTCATCT
                                  1 ATCGAAGGGTTCTGAGTCAFCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 07CG27 coding sequence.
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                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.2
Best Local Similarity 86.4
Matches 19; Conservative
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                         Human 07CG27 gene cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200116291-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999;
                                                                                                                                                                                                                                                                                                                              oncogene; ss.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                    23-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001
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                                                                                                                                                                                                  AAF28060;
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Matches
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ID. ABL7
XX ABL7
XX ABL7
DT 26-1
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                                                                                                                            RESULT 9
                                                                                                                                               AAF28060
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Helminth; aminopeptidase; H11-3; H11-2; H11-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding amino-peptidase from Haemonchus contortus and peptide(s) - useful in protective vaccines, for new transformed cells and oligosaccharide, for incorporation
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                                                 Score 17.2; DB 14; Length 3005; Pred. No. 44;
                                                                                       Indels
               Sequence 3006 BP; 932 A; 600 C; 716 G; 758 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3084 BP; 955 A; 610 C; 729 G; 790 T; 0 other;
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Pred. No. 44;
                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= H110D varient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
23..2956
                                                                                                                                                                                                                                                                                                                                                               Helminth aminopeptidase H11-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 75; 137pp; English.
                                                                                                                                               1429 ATCGAACGCTTCTGATACATCT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AGRI-) AGRIC & FOOD RES COUNCIL
                                                                                                                                                                                                                 RESULT 8
AAQ52500/c
ID AAQ52500 standard; DNA; 3084 BP.
                                                                                                                          1 ATCGAACGGTICTGAGTCATCT 22
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86.4%;
                                                 78.2%;
86.4%;
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                                                                                                                                                                                                                                                                                                                            (first entry)
                                                   Query Match 78.2
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knox DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-386574/48.
P-PSDB; AAR51282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in virus or microbe
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-1992;
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Smith TS;
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New DNA vectors,

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Gaps

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Indels

Length 10347;

DB 22;

03-JAN-2002

gene; ds

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrimer's disease, AlbS, epliepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%; Score 17.2; DB 24; Length 13202; larity 86.4%; Pred. No. 54; Conservative 0; Mismatches 3; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13202 BP; 3984 A; 187 C; 2851 G; 6180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1458; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein 5' EST, SEQ ID NO: 31408.
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                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8259 ATCGAACGATTCTAAATCATCT 8238
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                                                                                                                                                                                                        30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                           02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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Matches 19; Conserv
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                                                                  WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
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                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-0CT-2000
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                                                                                                              03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
AAC27333/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/alcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antifitamatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemnia; Alzabimer's disease; ALDS; epilepsy; eucrfibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarthritic; antidiabetic; attipsoriatic; antisoriatic; antiarthritic; antidiabetic; antisporiatic; antiarthritic; antidiabetic; antientisoriatic; anti-tinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                    Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24; Length 13202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13202 BP; 3470 A; 187 C; 2897 G; 6648 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                       Human immune system associated gene SEQ ID NO: 1457.
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0; Mismatches
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86.4%; Pred. No. 54
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01-SEP-2000; 2000DE-1043826.
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Matches 19; Conservative
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ABL33485;

ABL33485/c RESULT 11

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Query Match

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990S-0140353.
990S-0140695.
990S-0140695.
990S-0140991.
990S-0141287.
   9905 - 0132486 - 9905 - 0132487 - 9905 - 0134268 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 01324218 - 9905 - 01324218 - 9905 - 01324218 - 9905 - 01324218 - 9905 - 01324218 - 9905 - 01324218 - 9905 - 0132452 - 9905 - 0132452 - 9905 - 0132452 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 0132455 - 9905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 905 - 
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99US-0142055.
99US-0142390.
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99US-0144005.
99US-0144085.
99US-0144086.
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99US-0144331.
99US-0144332.
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99US-0139462.
99US-0139463.
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99US-0142920
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99US-0139763
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07-JUN-1999;
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24-MAY-1999;
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      The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTS sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from RNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                           Sequence 388 BP; 130 A; 55 C; 80 G; 123 T; 0 other;
                                                                  Claim 1; SEQ ID 31408; 71pp + CD-ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 TCTAACTGTACTGAGTCATCT 270
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99US-0127462.
99US-0128234.
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99US-0123548.
99US-0125788.
99US-0126264.
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99US-0132484.
99US-0132485.
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99US-0132048.
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Matches 18; Conservative
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29-MAR-1999;
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05-MAY-1999;
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21-APR-1999;
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06-APR-1999;
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23-MAR-1999
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9905-0151080
9905-0151303
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9905-0152363
9905-0153758
9905-0154018
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9905-0154039
9905-0154739
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990S-0158232.
990S-0158369.
990S-0159293.
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99US-0160768.
99US-0160770.
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9905-0149930.
9905-0150566.
9905-0150866.
9905-0151065.
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99US-0155659.
99US-0156458.
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99US-0157117.
99US-0157753.
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99US-0147416.
99US-014793.
99US-0148171.
99US-0148319.
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990S-0149864.
990S-0149368.
990S-0149175.
990S-0149722.
990S-0149723.
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99US-0159331.
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99US-0159329
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99US-0159638
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99US-0147260.
                     99US-0145218
                                    99US-0145276.
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                                                                                 990S-0146388
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21-0CT-1999;
21-0CT-1999;
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14-0CT-1999;
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20-SEP-1999;
22-SEP-1999;
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26-701-1999;
27-701-1999;
27-701-1999;
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11-AUG-1999;
12-AUG-1999;
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13-AUG-1999;
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17-AUG-1999;
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15-SEP-1999;
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29-SEP-1999;
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06-AUG-1999;
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09-AUG-1999;
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27-AUG-1999;
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01-SEP-1999;
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27-AUG-19
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                  Score 16.2; DB 21; Length 458; Pred. No. 1.1e+02;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                    ; LL
1.1e+02;
3;
                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 13074.
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                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      ABV13083 standard; cDNA; 470 BP
                                                                                                                                                                                                                                                               362 TCGACCGGTTCGGCGTCATCT 382
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85.7%;
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25-MAY-2000; 2
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16-JUL-19
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08-JUL-19
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               selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                            Gaps
                                                                          patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
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                                                                                                                                         73.6%; Score 16.2; DB 23; Length 470;
85.7%; Pred. No. 1.18+02;
Live 0; Mismatches 3; Indels 0.
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                                                                                                                                                             Local Similarity 85.7
hes 18; Conservative
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08-APR-1999;
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PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147105.

PR 10-AUG-1999; 99US-0147105.

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Search completed: January 9, 2003, 21:33:51 Job time : 16.4381 secs

Sequence 1, Appli Sequence 14, Appl Sequence 24, Appl Patent No. 5240838 Patent No. 5240838 Sequence 2, Appli

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2, Appli 204, App 5, Appli 5, Appli 7, Appli 72, Appli 22, Appli 4, Appli 4, Appli 6, Appli 7, Appli

Sequence 7 Sequence 2 Sequence 2

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APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDRAND ALBERT
APPLICANT: MUNN, DAYID PATRICK
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN BLIAABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AND THEIR USE IN THE PREPARATION (TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBW PC compatible
COMPUTER: TBW PC compatible
COMPUTER: TBW PC compatible
COMPUTER: TBW PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILLING DATE: 09-UAN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
US-08-828-451-1

US-09-134-078-14

US-09-1134-078-14

US-09-1134-078-14

524(08.8-1.3

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US-07-52-920-2

US-08-58-920-2

US-09-193-3778-5

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US-09-113-478-5

US-08-458-434A-7

US-08-458-434A-7

US-09-453-7028-72

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US-09-411-4658-4

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APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATE: 06-MAY-1993
FILING DATE: 06-MAY-1992
APPLICATION NUMBER: GB 920996
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, BAIDATA W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08335844A Patent No. 6066503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D. C.
                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6066503
GENERAL INFORMATION:
  US-08-335-844A-6/c
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                   GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-328-986-51
US-09-328-986-51
US-09-328-986-51
US-09-328-986-884-12
US-09-328-451-25
US-08-828-451-23
US-08-828-451-23
US-08-828-451-338-38
US-08-828-451-338-38
US-08-828-451-338-38
US-08-828-451-338-38
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US-08-828-451-338-38
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US-08-828-451-18
US-08-541-033A-1
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          1 atcgaacggttctgagtcatct 22
                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                        US-09-581-500B-13
22
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Match Length
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11506
11506
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11740
11969
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2137
2137
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                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                               Perfect score:
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Database :

Sequence:

Run on:

Searched:

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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 1100//1020
CURRENT PLILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFWARE: FastsEQ for Windows Version 3.0
LENGTH: 461
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: 1999-01-12
NUMBER OF SEQ. ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.6; DB
Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08387707
Patent No. 6265563
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KETTH, DUANE E.
TITLE OF INVENTION: OPIDID RECEPTOR GENES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/09228986 Patent No. 6359198
                                                                                                                                                  ; Sequence 55, Application US/09228986
; Patent No. 6359198
                               1429 ATCGAACGCTTCTGATACATCT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 ATCGAAGGCTCTGAGTCCACT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ATCGAAGGCTCTGAGTCCACT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATCGAACGGTTCTGAGTCATCT 22
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      1 ATCGAACGGTTCTGAGTCATCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.9%; Best Local Similarity 81.8%; Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) TYPE: DNA
) ORGANISM: Eucalyptus grandis
US-09-228-986-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-387-707-12/c
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US-09-228-986-51/c
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MINN, EDWARD ALBERT
KNOX, DAVID PATRICK
OLLYER, JOANNA JANE
NEWTON, SUSAN ELIZABETH
VEWTON, SUSAN ELIZABETH
VEWTION: ARROWEPTIDAE BNZYMES AND THERR USE IN THE PREPARATION OF
VENTION: VACCINES AGAINST HELMINTH INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                       Gaps
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                                                                                                        78.2%; Score 17.2; DB 3; Length 1689; 86.4%; Pred. No. 5.1;
                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
CURRENT APPLICATION DATE:
FILING DATE: 09-JAN-1995
CLASSIFTCATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: GB PWAY-1993
PRIOR APPLICATION NUMBER: GB 920936
FILING DATE: TO B-MAY-1993
APPLICATION NUMBER: GB 920936
FILING DATE: TO B-MAY-1993
ATTONEY AGENT INPOMMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
STREET: SLILE 701-E, 555 Thirteenth St., N.W.
                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-335-844A-19/c
; Sequence 19, Application US/08335844A
; Patent No. 6066503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEBRA: (202)783-6040
TELEFRA: (202)783-6031
INFORMATION FR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3084 base pairs
                                                                                                                                                                                                                     505 ATCGAACGCTTCTGATACATCT 484
                                                                                                                                                                                             1 ATCGAACGGTTCTGAGTCATCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                  19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                              Best Local Similarity
Matches 19; Conserv
; MOLECULE TYPE: 1; HYPOTHETICAL: NV; ANTI-SENSE: NO US-08-335-844A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE: NO US-08-335-844A-19
                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washin
STATE: D. C
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                             Query Match
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Sequence 80, Application US/09270542

| Sequence 80, Application US/09270542
| Patent No. 6322976
| GENERAL INFORMATION:
| APPLICANT: Altuman, Timothy
| APPLICANT: Scott, James
| APPLICANT: Stanton, Lawrence
| TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
| TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
| TITLE NEFERENCE: 4198/78179
| FILE REFERENCE: 4198/78179
| CURRENT FILING DATE: 1999-321/222
| CURRENT FILING DATE: 1999-12-23
| SAFIARE PAPLICATION NUMBER: 09/221,222
| SAFIARE: Patentin Ver: 2.0
| SSEQ ID NOS: 207
| SSEQ ID NOS: 207
| SSEQ ID NOS: 207
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-542-91/c

| Sequence 91, Application US/09270542
| Sequence 91, Application US/09270542
| Patent No. 6322946
| GENERAL INFORMATION:
| APPLICANT: Stort, James
| TITLE OF INVENTION: Therapy
| TITLE OF INVENTION: Therapy
| TITLE OF INVENTION: Therapy
| TITLE OF INVENTION: 1999-03-17
| CURRENT FILING DATE: 1999-12-23
| WINBER OF SEQ ID NOS: 207.
| SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                       70.9%; Score 15.6; DB 4; Length 2447; 81.8%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1436;
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Pred. No. 56;
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.1%; Score 15.2; 85.0%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                      750 ATCAAGTGGTTCTGACTCATCT 729
                                                                                                                                                                                                                                                                          1 ATCGAACGGTTCTGAGTCATCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.1%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TCGAACGGTTCTGAGTCATC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Rattus norvegicus US-09-270-542-89
                       LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                                                                                                               Sest_Local Similarity 81.8
Matches 18; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                  linear
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US-09-270-542-89/c
                                                                                               ; TOPOLOGY:
US-08-405-271A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 91
LENGTH: 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-542-91
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                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Sequence 12, Application US/08405271A

Patent No. 6432505

GENERAL INFORMATION:

APPLICANT: EVANS, CHRISTOPHER J.

APPLICANT: KEITH, DUANE E.

TITLE OF INVENTION: OPIOLD RECEPTOR GENES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSET: MORRISON & FOERSTER

STREET: 2000 PENNSTIVANIA AVENUE, NW, Suite 5500

CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MASHINGTON
STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20006-1888
COMPUTER: FLOPPY disk
COMPUTER: TAN PC Compatible
COMPUTER: TAN PC COMPATIBLE
COMPUTER: TAN PC POSYMS-DS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-MAR-1995
CLASSIFICATION HORBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION HUMBER: 22000-20526.22
TELECOMMUNICATION HUMBER: 22000-20526.23
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: 90-4030 MASINFORRAWIN
TELEPHONE: 90-4030 MASINFORRAWIN
INFORMATION FOR SEQ ID NO: 12:
                         2000 Pennsylvania Avenue, N.W. Suite 5500
                                                                                             COUNTRY: USA
ZIP: 20006-1888
ZORPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURSAHIGE, KATE H.
REGISTRATION NUMBER: 29,99
REFERENCE/DOCKET NUMBER: 22000-20526.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.6; DE
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,707
PILING DATE: 10-SEP-1995
CLASSIFICATION: 536
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      750 ATCAAGTGGTTCTGACTCATCT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATCGAACGGTTCTGAGTCATCT
                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-387-707-12
                                                   CITY:
STATE:
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QYg

Matches

g G

Q

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GENERAL INFORMATION:
APPLICANT: LYND DOUGETLE-Stamm et al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCK
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREMENCE: GTC-OMB: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Marison, James D
APPLICANT: Marison, James D
APPLICANT: Marison, James D
APPLICANT: Musicon, James D
APPLICANT: Musicon, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: DP. 1000.1050ul
CURRENT PAPLICATION NUMBER: US./09/724,864
PRIOR APPLICATION NUMBER: U.S. NO. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DB
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
SEQ ID NO 1980
LENGTH: 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-114-001C-1980/c
Facel 1980, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208, Application US/09149476; Patent No. 6420526; GENERAL INFORMATION:
                                                                                                                                      Sequence 12, Application US/09724864 Patent No. 6380362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1140 ATTARACGTTGTAAGTCATC 1120
    1146 TCGATAGGTTCTGAGACATC 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATCGAACGGTTCTGAGTCATC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AACAGGTCTGAGTCATCT 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.48
Best Local Similarity 81.07
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.3
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mouse US-09-724-864-12
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US-09-149-476-208
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    Gaps
                                                                                                                                                                                                                                                                                                                      APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REPERENCE: 4198/78L7
CURRENT APPLICATION NUMBER: 05/09/270,542
CURRENT APPLICATION NUMBER: 099-217
EARLIER APPLICATION NUMBER: 09/221,222
EARLIER PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Aituan, Timothy
APPLICANT: Scott, James
APPLICANT: Stanton, Lawrence
APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 4198/78179
CURRENT APPLICATION NUMBER: US/09/270,542
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CTHER INFORMATION: The N at positions 540, 546, and 550 can be any OTHER INFORMATION: nucleotide because the author is unsure of the corner information: exact sequence at these positions.
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  3; Indels
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Pred. No. 61;
0; Mismatches
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Pred. No. 57;
0; Mismatches
  Mismatches
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EARLIER APPLICATION NUMBER: 09/221,222
EARLIER FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                            RESULT 9
US-09-270-542-87/c
; Sequence 87, Application US/09270542
; Patent No. 6322976
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Patent No. 6322976
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                                                                        1113 TCGATAGGTTCTGAGACATC 1094
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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85.0%;
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                                                2 TCGAACGGTTCTGAGTCATC 21
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; ORGANISM: Rattus norvegicus
US-09-270-542-85
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Best Local Similarity 85.0
Matches 17; Conservative
17; Conservative
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Aitman, Timothy
APPLICANT: Scott, James
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LENGTH: 2436
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FEATURE:

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CHREEN FILING DATE. 1939-00-185-40493

BARLIER PLING DATE. 1939-00-185-40493

BARLIER PLING DATE. 1939-00-185-40493

BARLIER PLING DATE. 1939-00-10-185-40493

BARLIER PRILOKON NUMBER: 60/04, 334

BARLIER APPLICATION NUMBER: 60/04, 336

BARLIER PRELOKON NUMBER: 60/04, 536

BARLIER PRELOKON NUMBER: 60/04, 537

BARLIER PRELOKON NUMBER

BARLIER APPLICATION NUMBER: 60/043,674
EBALIER PILING DATE: 1997-04-11
EBALIER PILING DATE: 1997-04-12
EBALIER PILING DATE: 1997-06-22
EBALIER PILING DATE: 1997-06-22
EBALIER PILING DATE: 1997-06-22
EBALIER PILING DATE: 1997-08-22
EBALIER PILING DATE: 19

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Sequence 25, Application US/08628451

Sequence 25, Application US/08628451

Setent No. 5985634

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
ITILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
ITILE OF INVENTION: DEHYDROGENASES AND SUBUNITS OF GLUTAMATE
ITILE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREFT: S421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
COUNTRY: USA
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Pred. No. 1.2e+02;
0; Mismatches 4; Indels 0
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                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
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APPLICATION NUMBER: US/08/541,033
FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      ATTORNEY FAGRET INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
REMORTATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 Base Pairs
TYPE: NUCLEIC SCHOOLE
STRANDEDNESS: GOUDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1261 reargegerreregerearer 1241
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Best Local Similarity 81.0%;
Matches 17; Conservative (
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                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
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MOLECULE TYPE: CDNA
Gainesville
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                             Florida
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US-08-541-033A-25
                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/056,875
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APPLICATION NUMBER: 60/056,887
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APPLICATION NUMBER: 60/056,908
                    APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23
                                                                                                                                                                                       APPLICATION NUMBER: 60/047,593
FILING DATE: 1997-05-23
                                                                                                                                                                                                                    FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
                                                                                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/043,670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
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APPLICATION NUMBER: 60/048,964
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                                                                                                                                     APPLICATION NUMBER: 60/047,589
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/043,576
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/047,501
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                                                                               60/047,594
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; Sequence 25, Application US/08541033A
; Patent No. 5879941
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Best Local Similarity 81.05
Matches 17; Conservative
                                                                               APPLICATION NUMBER:
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TITLE OF INVENTION: REL.
TITLE OF INVENTION: DEH
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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2: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389086 seqs, 220051671 residues
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Maximum Match 100%
Listing first 45 summaries
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22
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 421, App	Sequence 20, Appl	Sequence 22, Appl	Sequence 30, Appl	Sequence 461, App	Sequence 2640, Ap	Sequence 12, Appl	Sequence 544, App	Sequence 44, Appl	Sequence 580, App	Sequence 499, App	Sequence 5, Appli	Sequence 3, Appli	Sequence 94, Appl	Sequence 777, App	Sequence 2536, Ap	Sequence 2544, Ap	Seguence 13, Appl	Sequence 146, App
	3 ID	9 US-09-938-842A-421	10 US-09-775-879-20	10 US-09-775-879-22	10 US-09-974-300-30	10 US-09-294-093B-461	9 US-09-938-842A-2640	10 US-09-823-114-12	10 US-09-925-301-544	9 US-10-071-766-44	10 US-09-925-300-580	10 US-09-917-800A-499	10 US-09-747-835A-5	10 US-09-747-835A-3	10 US-09-070-927A-94	10 US-09-764-860-777	10 US-09-764-877-2536	10 US-09-764-877-2544	9 US-10-135-322-13	10 US-09-764-877-146
	Length DB	846	1889	2925	1293	292	2313	2447	3109	3954	4006	1469	2484	3188	21252	23934	23934	23934	70768	510
οP	Query Match	78.2	78.2	78.2	71.8	70.9	70.9	70.9	70.9	70.9	70.0	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	68.2
	Score	17.2	17.2	17.2	15.8	15.6	15.6	15.6	15.6	15.6	15.4	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15
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Gaps 0;

ch 78.2%; Score 17.2; DB 9; Length 846; I Similarity 86.4%; Pred. No. 8.1; 19; Conservative 0; Mismatches 3; Indels (

Query Match Best Local Similarity

Matches

TYPE: DNA ORGANISM: Arabidopsis thaliana

US-09-938-842A-421

1 ATCGAACGGIICTGAGICAICT 22 . 56 ACCGAATCGTTCTGAGTCATCT 77 Sequence 20, Application US/09775879; Patent No. US200200068822Al GENERAL INFORMATION: APPLICANT: Choe, Sunghwa

US-09-775-879-20

RESULT 2

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Sequence 2302, Ap Sequence 155, App Sequence 155, App Sequence 2301, Ap Sequence 2014, Ap Sequence 1094, Ap Sequence 1094, Ap Sequence 1094, Ap Sequence 1094, Ap Sequence 1121, Ap Sequence 1121, Ap Sequence 1124, Ap Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 264, App Sequence 264, App Sequence 264, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 27, Appli Sequenc	TRANSGENIC PLANTS CONTAININ
0 US-09-764-877-2302 0 US-09-938-842A-155 0 US-09-938-876-2317 0 US-09-932-876-2317 0 US-09-932-876-2317 0 US-09-932-876-1094 US-09-932-947-1094 US-09-932-947-1094 US-09-931-842-502 0 US-09-931-842A-1129 US-09-938-842A-1129 US-09-938-842A-1129 US-09-938-842A-1129 US-09-938-842A-1129 US-09-938-844-23 US-09-938-844-23 US-09-938-842A-6419 US-09-070-844-13 US-09-070-844-13 US-09-070-844-13 US-09-070-844-13 US-09-070-844-13 US-09-070-844-13 US-09-070-844-13 US-09-070-844-13 US-09-070-844-18 US-09-070-844-18 US-09-070-844-18 US-09-070-844-18	ALIGNMENTS 09938842A EGULATED GENES OF PLANTS, ND METHODS OF USE 05/09/938,842A 8-24 60/227,866 4 60/227,866 60/300,111
15 68.2 1868 10 14.8 66.4 258 10 14.6 66.4 4258 10 14.6 66.4 4258 10 14.6 66.4 610 9 14.6 66.4 610 9 14.6 66.4 610 9 14.6 66.4 610 9 14.6 66.4 1107 9 14.6 66.4 1187 10 14.6 66.4 1288 10 14.6 66.4 2098 10 14.6 66.4 2099 10	ALIGNMENTS RESULT 1 US-09-938-842A-421 Sequence 421, Application US/09938842A Patent No. US202020160338A1 APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel APPLICANT: Wang, Xun APPLICANT: Zhu, Tong TITLE OF INVENTION: SAME, AND METHODS OF USE TITLE OF INVENTION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR PRILING DATE: 2000-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 20
0000 00 0 00 0 00000000000000000000000	RESULT 1 US-09-938-84 ; Sequence 4 ; Patent No. ; GENERAL IN ; APPLICANY ; TITE OF ; TIT

Database :

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APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF THE REPRENCE: SCRIPISON-08-24
PRIOR PLILING DATE: 2000-08-24
PRIOR PLILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ito, Laura, Y. APPLICANT: Ito, Laura, Y. APPLICANT: Sherman, Bradley, K. TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED PROM CORN TASSEL TILE REFERENCE: PL-0009 US CURRENT APPLICATION NUMBER: US/09/294,093B
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: APFIL 21, 1998
NUMBER OF SEQ ID NOS: 6207
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                                                                                                                                                                      0;
                                                                                                                        DB 10; Length 1293;
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700342780H1
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                                                                                                                      Score 15.8; DB
Pred. No. 46;
0; Mismatches
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81.8%; Pred. No. 47;
tive 0; Mismatches
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LOCATION: 266-267

CHERR INFORMATION: a, t, c, g, or other

US-09-294-093B-461
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US-09-938-842A-2640
y Sequence 2640, Application US/09938842A
y Patent to US20020160378A1
SENERAL INPORMATION:
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US-09-294-093B-461/c
; Sequence 461, Application US/09294093B
; Gartent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 ALCAAACGGGTTTGAGTAATCT 233
                            ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-30
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89.5%;
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                                                                                                                   Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
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Best Local Similarity
Matches 18; Conserv
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ORGANISM: Zea mays
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SEQ ID NO 461
LENGTH: 292
         LENGTH: 1293
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Pred. No. 9.8;
0; Mismatches 3; Indels 0:
                                                                                                                                                                                                                                                                                                                                                   Length 1889;
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1b Groth
ITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PILIG DAIE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
                                                                                                                                                                                                                                                                                                                                               Query Match 78.2%; Score 17.2; DB 10; Best Local Similarity 86.4%; Pred, No. 9.1; Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09775879;
Patent No. US20020068822a1
GENERAL INFORMATION:
APPLICANT: Choe, Sunghwa
APPLICANT: Feldmann, Kenneth A
TITLE OF INVENTION: Dwf7 MUTANTS
TITLE OF INVENTION: Dwf7 MUTANTS
CURRENT APPLICATION NUMBER: US/09/775,879
CURRENT APPLICATION NUMBER: 60/179,901
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 22
IENGTH: 2925
APPLICANT: Feldmann, Kenneth A
TITLE OF INVENTION: Dwf7 MUTANTS
FILE REPERENCE: 2225-0063
CURRENT APPLICATION NUMBER: US/09/775,879
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/179,901
PRIOR APPLICATION NUMBER: 60/179,901
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1889
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PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OS SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Genomic dwf7 (Arabidopsis)
US-09-775-879-20
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Best Local Similarity 86.4%;
Matches 19; Conservative
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; ORGANISM: Genomic HDF7
US-09-775-879-22
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US-09-775-879-22
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPERENCE: PAIGO.
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-33-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SEQ ID NO 544
LENGTH: 3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020192678A1 251859.2
NAME/KEY: unsure
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TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
FILE REFERRNCE: PA-0043 US
CURRENT APPLICATION NUMBER: US/10/071,766
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PERL Program
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Pred. No. 66;
O; Mismatches
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; OTHER:INFORMATION: a, t, c, g, or other
US-10-071-766-44
                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1011)
; OTHER INFORMATION: n equals a,t,g; or c
US-09-925-301-544
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; Patent No. US20020151681A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/10071766 Publication No. US20020192678A1 GENERAL INFORMATION:
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ilarity 81.8%;
Conservative C
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81.8%;
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Best Local Similarity 81.55,
Thes 18; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Craig Rosen,
                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
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LENGTH: 3954
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                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                     DB 9; Length 2313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                            4; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KAPE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EVANS, CHRISTOPHER J.

TITLE OF INVENTION: OPICID RECEPTOR GENES
NUMBER OF SEQUENCES: 25
                                                                                                     Score 15.6; DB
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/148,351
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERA: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
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Patent No. US20020052308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY GISK
                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09823114 Patent No. US20020061554A1 GENERAL INFORMATION:
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LENGTH: 2447 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                            ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2640
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81.8%;
                                                                                                   Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                      US-09-823-114-12/c
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US-09-925-301-544
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        LENGTH: 2313
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APPLICANT: ASUMIL, VINOR
APPLICANT: ASUMIL, VINOR
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLECTIDES
TITLE REPERRENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/99/747,835A
CURRENT FILING DATE: 2000-13-08
PRIOR PELICATION NUMBER: US 09/653,450
PRIOR PELICATION NUMBER: US 09/653,450
PRIOR PLILING DATE: 2000-08-31
PRIOR PLILING DATE: 2000-08-31
PRIOR PLILING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-20
PRIOR PLILING DATE: 2000-06-20
PRIOR PLILING DATE: 2000-04-25
PRIOR PRIOR PLILING DATE: 2000-04-25
PRIOR PRIOR PLILING DATE: 2000-04-25
PRIOR PLILING DATE: 2000-04-25
PRIOR PRIOR PLILING DATE: 2000-04-25
PRIOR PRIOR PLILING DATE: 2000-04-25
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-1
TITLE OF INVENTION: LIKE) POLYEPPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.1%; Score 15.2; DB 10; Length 2484;
85.0%; Pred. No. 1e+02;
Live 0; Mismatches 3; Indels 0;
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PRIOR FILINE DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09747835A Patent No. US20020146692A1
                                                                                                                    Sequence 5, Application US/09747835A Patent No. US20020146692A1
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APPLICANT: Yamazaki, Victoria
                                                                                                                                                                                                                          APPLICANT: Yamazaki, Victoria APPLICANT: Tang, Y. Tom
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Best Local Similarity 85.0°
Matches 17; Conservative
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Liu, Chenghua
Zhou, Ping
Wang, Dunrui
Shang, Jie
Ren, Reiyan
Asundi, Vinod
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Ren, Feiyan
Asundi, Vinod
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Liu, Chenghua
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Wang, Dunrui
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; ORGANISM: Homo sapiens
! US-09-747-835A-5
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LENGTH: 2484
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-09-917-800A-499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4; DB 10; Length 4006;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05988
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SEQ ID NO 580
LENGTH: 4006
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Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
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94.1%;
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Best Local Similarity 94.1;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-300-580
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US-09-917-800A-499/c
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US-09-764-860-777/C
: Sequence 777, Application US/09764860
: Patent No. US20020094953A1
: GENERAL INFORMATION:
: APPLICANT: ROSEON et al.
: TILLE OF INVENTION:
: TILLE PREPRENCE: PCOOR
: CURRENT APPLICATION NUMBER: US/09/764,860
: SOUTHENT ELINE DATE: 2001-01-17
: NUMBER OF SEQ ID NOS: 1198
: SOFTWARE: PATENTIN Ver. 2.0
: SEQ ID NO 777
                                                                                  Query Match 69.1%; Score 15.2; DB 10; Length 21252; Best Local Similarity 85.0%; Pred. No. 1.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0;
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                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-070-927A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 10, 2003, 06:43:17 Job time : 8.87949 secs
                                                                                                                                                                                                     DD 10687 TCAAACTGTTCTGATTCATC 10706
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                                                                                                                                                                             2 TCGAACGGTTCTGAGTCATC 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.18
Best Local Similarity 85.09
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-860-777
                                                                                                                                                                     $ QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 94, Application US/09070927A.
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VETSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
                                                                                                                                                                                                                                                                                                                                                                                                                              69.1%; Score 15.2; DB 10;
85.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNET/AGENT INFORMATION:
NAME: REALLY HOOVER: AB369
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8504
TELEPAX: (301) 309-8504
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 3
LENGTH: 3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 21252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CGAACGGTTCTGAGTCATCT 22
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.09
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(2484)
US-09-747-835A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-070-927A-94
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BE318984 NF043F02L
BG4449328 NF043F021
BG4467650 NB_13_O1D
BH990723 BOHIET37F
AQ957346 LERAP27TF
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BF989989 CM3-WT019
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BF738261 CM3-KT003
BG908704 KC2-GN026
BG00864 RC2-GN026
BG00864 RC2-GN026
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AQ05224 EST374297
AW76293 MRO-ST003
AW062934 MRO-ST003
AW062934 MRO-ST003
BF883208 QV3-ET017
AW77472 MRI-CT005
BF883208 QV3-ET017
AW77472 MRI-CT005
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AW762911 WA1269.X
AL670991 WA12709.X
BH883208 CM3-BT017
BH883208 CM3-BT017
AW7612114 AM3-AGF-BH883208 AG-WD-137
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BP002543 BP002543
AW994568 RCO-BN003
BF295216 014PbA02
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AW053439 L30-1352T
AL140234 Anopheles
BF529413 G02041936
AL149141 Anopheles
BF964582 602267886
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1 (bases 1 to 244)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 482 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                         AL152485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 bp mRNA linear ESI am38h04.s1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone AA889105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 482 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                               AW962224
AW266225
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BH383813
BH383813
AW994568
BF295216
AW2595216
AW053439
CNS01E8P
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BG008684
AQ914000
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CNS01L30
BF964582
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BF738261
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AW003072
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                                                                                               AW374777
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 Homo sapiens
human.
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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AA889105
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AA904435 ok07911.s
BG807824 NISC_KK10
BQ435307 AGENCOURT
BG452389 NF097F02L
BE999204 EST430927
                                                                      9, 2003, 21:14:32; search time 74.5156 Seconds (without alignments) 4781.561 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                              32308132
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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AA904435
BQ807824
BQ435307
BG452389
BE999204
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      1 ategaacggttctgagtcatct 22
                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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em_gss_mam:*
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em_estom:*
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em_gss_pln:
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em_htc:*
gb_est1:*
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em_estmu:*
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gb_htc:*
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gb_est4:*
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Match Length
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EST:*

Database

Scoring table:

Searched:

Perfect score: Sequence:

on:

Run

114. 1174. 1174. 1221. 1221. 124.

100.0 100.0 100.0 100.0 88.2

22 22 22 22 22 4.61

Score

Result М М $^{\circ}$

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Info@inage.llnl.gov
Plate: LLAMIS40 row: K column: 8
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                 BQ807824 636 bp mRNA linear EST 31-JUL-2002 NISC_Kk10f04.y1 NCI_CGAP_Brn72 Macaca mulatta cDNA clone IMAGE:5331199 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Macaca.

1. (bases 1 to 6.2)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hypothalamus"

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/host="Nabl0B (phage-resistant)"

/note="Organ: brain, Vector: pCMV-SPORM6.ccdb; Site_1:
Not1; Site_2: EcoRV; Cloned unidirectionally. Primer:
Not1; Site_2: EcoRV; Cloned unidirectionally. Primer:
Not1; Organ: Average insert size 2.2 kb. Constructed by
Invitrogen. Note: this is a NCL_CGAP Library."
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                           Indels
                         ;
  100.0%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Brn72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Macaca mulatta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Emall: Graphs-rémail.nih.gov
cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 ATCGAACGGTTCTGAGTCATCT 410
                                                                                        121 ATCGAACGGTTCTGAGTCATCT 142
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BQ435307.1 GI:21174383
                                                               22
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                                                                 1 ATCGAACGGITCIGAGICATCI
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Best Local Similarity 100...
Conservative
                         22; Conservative
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  Best Local Similarity
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BQ807824/c
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ORIGIN
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
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BQ435307
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SOURCE
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/lab_host="DH10B"
/note="Corpan: pooled, Vector: pT73D-Pac (Pharmacia) with
a host="Organ: pooled, Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_l: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH1109, testis NHT; and B-cell
NOT_CGAP GCBl) ware mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hypridization reaction. The driver
was PGR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399, Subtraction by Bento
Soares and M. Fatina Bonaldo.
                                    EST 09-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Insert Length: 437 Std Error: 0.00
Seq primer: 40ml3 fwd. Er from Amersham
High quality sequence stop: 232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA linear EST
Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 22; DB 9; Length 244; Best Local Similarity 100.0%; Pred. No. 3.6; Matches 22; Conservative 0; Mismatches 0; Indels
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/clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 bp

N ok07g11.s1 Soares_NFL_T_GBC_S1 Homc

IMAGE:1507172 3', mRNA sequence.

AA904435

AA904435.1 GI:3039558

EST.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1507172"
                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATCGAACGCTTCTGAGTCATCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCGAACGGTTCTGAGTCATCT 22
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AA904435
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KEYWORDS
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/tissue_tro__srenescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR" site_1: EcoRI; Site_2:
Xhol; CDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage. The
collected from 2 month old plants at mid-pod stage. The
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing CDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist helper phage and propagated in SOLR cells."
2 a 119 c 145 g 143 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE999204 1inear EST 06-OCT-2000 EST430927 GVSN Medicago truncatula cDNA clone pGVSN-15B23, mRNA
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
T=1: 612 625 5715
Fax: 651-649-5058
                /clone_lib="Developing leaf"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
114 c 94 g 99 t 3 others
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University of Minnesota name: M273182e TIGR sequence name:
MTKBA12TK More information is available at:
http://chrysle.tamu.edu/medicago
Seq primer: SKmod (CTA gAA)CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                      Length 408;
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/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                   Score 19.4; DB Pred. No. 76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="pGVSN-15B23"
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/clone="NF097F02LF"
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95.2%;
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Torres-Jerez, L., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosida I, Fabalas, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13511 row: p column: 22
High quality sequence stop: 607.
Location/Qualifiers
I. 930
/organism="Homo capiens"
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NF097F02LF1F1016 Developing leaf Medicago truncatula cDNA clone
                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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Insert Length: 408 Std Error: 0.00
Plate: 097 row: F column: 02
Seg primer: TCACACAGGAACAGCTATGAC.
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/clone="IMAGE:6160773"
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/db_xref="taxon:3880"
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BG452389
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  1 (bases 1 to 930)
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Query Match

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RESULT 7

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

JOURNAL

TITLE

FEATURES

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DOM#9328
NF043GOSINIF1038 Insect herbivory Medicago truncatula cDNA clone MF043GOSIN 5', mRNA sequence.
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May.G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Unpublished (2000)
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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                              Medicago.

1 (bases 1 to 653)

1 (bases -derez_I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
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/tissue_type="leaf"
/dev_stagg="Pooled developmental"
/dev_stagg="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
/young, developing, mature and senescing leaves."
                                                                                                                                                                                                                                             Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9192761
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Dept. of Plant Pathology
University of Armansas
217 Plant Science Building, Fayetteville, AR 72701, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: gdmay@noble.org
Medicago Genome Initiative accession: WGI:S:27143
Insert Length: 677 Std Error: 0.00
Enter: 043 row: F column: 02
Seq primer: TCACACAGGAAACAGCTAATGAC.
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7391
Fax: 580 221 7380
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Pred. No. 92;
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/db_xref="taxon:3880"
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Fax: 501 575 7601
Email: kkorth@ccmp.uark.edu
Insert Length: 668 Std Error: 0.00
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95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E (bases 1 to 632)
S Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores A.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Contact: Korth R
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Bullding, Payetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: Kkorth@comp.uark.edu
Insert Length: 632 Std Error: 0.00
                                                                                                                                                                                                                                          632 bp mRNA linear EST 19-DEC-2000 NF012C1ZINIF1087 Insect herbivory Medicago truncatula cDNA clone NF012C1ZIN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /close_lib="libsect herbivory"
/tissue_type="local and systemic leaves"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
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Medicago truncatula
Bukaryothyta; Embryophyta; Tracheophyta:
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta:
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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88.2%; Score 19.4; DB 12; Length 529; 95.2%; Pred. No. 85; 1; Indels 0. Mismatches 1; Indels 0.
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/db_xref="taxon:3880"
/clone="NF012C121N"
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Pred. No. 91;
0; Mismatches
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Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
1. .632
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ilarity 95.2%;
Conservative (
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                                                   Conservative
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Matches 20; Conserv
                 Best Local Similarity
Matches 20; Conserv
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ACCESSION VERSION KEYWORDS SOURCE

BE318984/c

RESULT 8

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BASE COUNT

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Gaps

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AQ957346 143 bp DNA linear GSS 28-JAN-2000 LERAP27TF LERA Arabidopsis thaliana genomic clone LERAP27, DNA
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thale cress.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                            BHS90723 773 bp DNA linear GSS 15-DEC-2001
BOHIE73TF BOHI Brassica oleracea genomic clone BOHIE73, DNA
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

Other_GSSs: HOHIE73TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/organism="Brassica oleracea"
/strain="T01000H3"
/db xef="taxon:3712"
/clone="BOHIE73"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 209 c 165 g 201 t
                                                                                                                                                           Gaps
Nottingham, UK) from mRNA from N.americanus L3 stage (Nottingham strain) maintained in hamsters."
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                                                                                                                Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850, USA. Teal: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF
Class: sheared ends.
                                                                                                                                                           2; Indels
                                                                                                              80.9%; Score 17.8; DB 12;
90.5%; Pred. No. 5.5e+02;
iive 0; Mismatches 2;
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                                                                                                                                                           19; Conservative
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                                                                                                                                       Best Local Similarity
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AQ957346/c
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                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DG467650 715 bp mRNA linear EST 21-MAR-2001 Na_LI3_01D05_SAC Necator americanus (parasitic nematode) L3 Necator americanus cDNA clone Na_LI3_01D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Necator americanus.
Necator americanus
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidaa; Ancylostomatidae; Bunostominae; Necator.
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                                                                                                                                                                                                            /dev_stage="mature"
/note="Vector: Lambda 2ap; Library was produced from fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 715)
Blaxter,M.L., Parkinson,J., Whitton,C., Daub,J., Guiliano,D., Hall
N., Quayle,N. and Barrell,B.
Edinburgh University/Sanger Centre Nematode EST Project
Unpublished (2000)
                                                                                                                                                                                                                                         expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

7 others
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/clone_lib="Necator americanus (parasitic nematode) L3"
/sex="Mixed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mark.blaxtereed.ac.uk
The library was prepared for Dr. David Pritchard University Of
Nottingham Sequencing was performed by Claire Whitton ICAPB,
Edinburgh
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 668;
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                                                                                         /organism="Medicago truncatula"
/db_xref="taxon:3880"
/db_xref="nF0436051N"
/clone_ib="insect herbivory"
/tissue_type="local and systemic leaves"
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Institute of Cell, Animal and Population Biology
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/db_xref="taxon:51031"
                                                                                                                                                                                                                                                                                                                                                                                                          88.2%; Score 19.4; D 95.2%; Pred. No. 93; tive 0; Mismatches
    Plate: 043 row: G column: 05
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Plate: 01 row: D column: 05
Seq primer: Seq
High quality sequence stop: 463.
Location/Qualifiers
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BG467650.1 GI:13418254
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Tel: +44 131 650 6760
Fax: +44 131 670 5450
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Matches 20; Conservative
                                                                         1.,668
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FORWARD: SAC
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BG467650/c
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Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 129
Location/Qualifiers
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86.4%;
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludaig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludaig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0195-051200-525-f04&t3=2000-12-05&t4=1)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. I (bases 1 to 143)
Buell, C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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CM3-MT0195-051200-525-f04 MT0195 Homo sapiens CDNA, mRNA seguence.
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/clone_libe_libra.
/clone_libe_libra.
/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp Defore ligation."
24 c 15 g 57 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Seg primer: TF
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Laboratory of Cancer Genetics
Ludvig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 143;
                                                                                                                                                                 Upublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
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Pred. No. 5.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
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/clone="LERAP27"
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86.4%;
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Best Local Similarity
Matches 19; Conserv
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/dev_stage="nature" //dev_stage="nature" //dev_stag
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.
1 (bases 1 to 349)
Dias Neto,E., Garcia Correa,R., Verjovski.Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. 1., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
.M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3et2=CM3.MT0195-051200-525-hl0&t3=2000-12-05&t4=1)
Seq primer: put 18 forward
High quality sequence start: 19
High quality sequence stop: 347.
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Sma1; A mini-library was made by cloning products derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 7.4e+02;
0; Mismatches 3;
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1. .298
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396 bp mRNA linear EST 10-JAN-2001 CM3-KT0033-151200-572-f10 KT0033 Homo sapiens cDNA, mRNA sequence. BF738194.1 GI:12064870 FSF
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1 (bases 1 to 366)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costas, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Seq primer: pur 18 forward
High quality sequence start: 5
High quality sequence start: 5
High quality sequence start: 5
from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 8.3e+02;
0; Mismatches 3;
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Pred. No. 7.8e+02;
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/clone_lib="KT0033"
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Email: asimpson@ludwig.org.br
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Best Local Similarity 86.4%;
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nes 19; Conservative
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Search completed: January 10, 2003, 06:15:19 Job time: 78.6156 secs